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<110> Bejanin, Stephan
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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Phe	Leu	Glu	Asp	Gly	Lys	Gly	Asn	Met	Asn	Cys	Ala	Tyr	Phe	His	Asn	
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His Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser			
35	40	45	
Phe Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu			
50	55	60	
Leu Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln			
65	70	75	80
Ala Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu			
85	90	95	
Lys Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser			
100	105	110	
Tyr Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val			
115	120	125	
Asn Lys Leu Leu Phe Ala Ala His Leu Pro Val Phe Thr Tyr Thr Glu			
130	135	140	
Gln His Ala Leu Leu Gln Asp Gln Pro Phe Ile Gln Asp Asp Cys Tyr			
145	150	155	160
Tyr His Gly Tyr Val Glu Gly Val Pro Glu Ser Leu Val Ala Leu Ser			
165	170	175	
Thr Cys Ser Gly Gly Phe Leu Gly Met Leu Gln Ile Asn Asp Leu Val			
180	185	190	
Tyr Glu Ile Lys Pro Ile Ser Val Ser Ala Thr Phe Glu His Leu Val			
195	200	205	
Tyr Lys Ile Asp Ser Asp Asp Thr Gln Phe Pro Pro Met Arg Cys Gly			
210	215	220	
Leu Thr Glu Glu Lys Ile Ala His Gln Met Glu Leu Gln Leu Ser Tyr			
225	230	235	240
Asn Phe Thr Leu Lys Gln Ser Ser Phe Val Gly Trp Trp Thr His Gln			
245	250	255	
Arg Phe Val Glu Leu Val Val Val Asp Asn Ile Arg Tyr Leu Phe			
260	265	270	

Ser Gln Ser Asn Ala Thr Thr Val Gln His Glu Val Phe Asn Val Val
 275 280 285
 Asn Ile Val Asp Ser Phe Tyr His Pro Leu Glu Val Asp Val Ile Leu
 290 295 300
 Thr Gly Ile Asp Ile Trp Thr Ala Ser Asn Pro Leu Pro Thr Ser Gly
 305 310 315 320
 Asp Leu Asp Asn Val Leu Glu Asp Phe Ser Ile Trp Lys Asn Tyr Asn
 325 330 335
 Leu Asn Asn Arg Leu Gln His Asp Val Ala His Leu Phe Ile Lys Asp
 340 345 350
 Thr Gln Gly Met Lys Leu Gly Val Ala Tyr Val Lys Gly Ile Cys Gln
 355 360 365
 Asn Pro Phe Asn Thr Gly Val Asp Val Phe Glu Asp Asn Arg Leu Val
 370 375 380
 Val Phe Ala Ile Thr Leu Gly His Glu Leu Gly His Asn Leu Gly Met
 385 390 395 400
 Gln His Asp Thr Gln Trp Cys Val Cys Glu Leu Gln Trp Cys Ile Met
 405 410 415
 His Ala Tyr Arg Lys Val Thr Thr Lys Phe Ser Asn Cys Ser Tyr Ala
 420 425 430
 Gln Tyr Trp Asp Ser Thr Ile Ser Ser Gly Leu Cys Ile Gln Pro Pro
 435 440 445
 Pro Tyr Pro Gly Asn Ile Phe Arg Leu Lys Tyr Cys Gly Asn Leu Val
 450 455 460
 Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Thr Ile Arg Gln Cys Ala
 465 470 475 480
 Lys Asp Pro Cys Cys Leu Leu Asn Cys Thr Leu His Pro Gly Ala Ala
 485 490 495
 Cys Ala Phe Gly Ile Cys Cys Lys Asp Cys Lys Phe Leu Pro Ser Gly
 500 505 510
 Thr Leu Cys Arg Gln Gln Val Gly Glu Cys Asp Leu Pro Glu Trp Cys
 515 520 525
 Asn Gly Thr Ser His Gln Cys Pro Asp Asp Val Tyr Val Gln Asp Gly
 530 535 540
 Ile Ser Cys Asn Val Asn Ala Phe Cys Tyr Glu Lys Thr Cys Asn Asn
 545 550 555 560
 His Asp Ile Gln Cys Lys Glu Ile Phe Gly Gln Asp Ala Arg Ser Ala
 565 570 575
 Ser Gln Ser Cys Tyr Gln Glu Ile Asn Thr Gln Gly Asn Arg Phe Gly
 580 585 590
 His Cys Gly Ile Val Gly Thr Thr Tyr Val Lys Cys Trp Thr Pro Asp
 595 600 605
 Ile Met Cys Gly Arg Val Gln Cys Glu Asn Val Gly Val Ile Pro Asn
 610 615 620
 Leu Ile Glu His Ser Thr Val Gln Gln Phe His Leu Asn Asp Thr Thr
 625 630 635 640
 Cys Trp Gly Thr Asp Tyr His Leu Gly Met Ala Ile Pro Asp Ile Gly
 645 650 655
 Glu Val Lys Asp Gly Thr Val Cys Gly Pro Glu Lys Ile Cys Ile Arg
 660 665 670
 Lys Lys Cys Ala Ser Met Val His Leu Ser Gln Ala Cys Gln Pro Lys
 675 680 685
 Thr Cys Asn Met Arg Gly Ile Cys Asn Asn Lys Gln His Cys His Cys
 690 695 700
 Asn His Glu Trp Ala Pro Pro Tyr Cys Lys Asp Lys Gly Tyr Gly Gly
 705 710 720

Ser Ala Asp Ser Gly Pro Pro Pro Lys Asn Asn Met Glu Gly Leu Asn
 725 730 735
 Val Met Gly Lys Leu Arg Tyr Leu Ser Leu Leu Cys Leu Leu Pro Leu
 740 745 750
 Val Ala Phe Leu Leu Phe Cys Leu His Val Leu Phe Lys Lys Arg Thr
 755 760 765
 Lys Ser Lys Glu Asp Glu Glu Gly
 770 775

<210> 7
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..263

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 <222> 264..926

<220>
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 <222> 927..1436

<220>
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 <222> 1404..1409

<220>
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 <222> 1421..1436

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 gcagggcaaa cactgaggtc aactacaagc cacaggcccc ttcccccagcc tcagttcaca 180
 gctgccctgt tgcagggagg cggtggccct tctgttgcata gaccgagcct gtggatata 240
 ccaaggcaga ggagccata gcc atg agg agc ctc ggg gcc ctg ctc ttg ctg 293
 Met Arg Ser Leu Gly Ala Leu Leu Leu
 -15 -10
 ctg agc gcc tgc ctg gcg gtg agc gct ggc cct gtg cca acg ccg ccc 341
 Leu Ser Ala Cys Leu Ala Val Ser Ala Gly Pro Val Pro Thr Pro Pro
 -5 1 5
 gac aac atc caa gtg cag gaa aac ttc aat atc tct cgg atc tat ggg 389
 Asp Asn Ile Gln Val Gln Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly
 10 15 20
 aag tgg tac aac ctg gcc atc ggt tcc acc tgc ccc tgg ctg aag aag 437
 Lys Trp Tyr Asn Leu Ala Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys
 25 30 35
 atc atg gac agg atg aca gtg agc acg ctg gtg ctg gga gag ggc gct 485
 Ile Met Asp Arg Met Thr Val Ser Thr Leu Val Leu Gly Glu Gly Ala
 40 45 50 55
 aca gag gcg gag atc agc atg acc agc act cgt tgg cgg aaa ggt gtc 533
 Thr Glu Ala Glu Ile Ser Met Thr Ser Thr Arg Trp Arg Lys Gly Val

60	65	70	
tgt gag gag acg tct gga gct tat gag aaa aca gat act gat ggg aag			581
Cys Glu Glu Thr Ser Gly Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys			
75	80	85	
ttt ctc tat cac aaa tcc aaa tgg aac ata acc atg gag tcc tat gtg			629
Phe Leu Tyr His Lys Ser Lys Trp Asn Ile Thr Met Glu Ser Tyr Val			
90	95	100	
gtc cac acc aac tat gat gag tat gcc att ttc ctg acc aag aaa ttc			677
Val His Thr Asn Tyr Asp Glu Tyr Ala Ile Phe Leu Thr Lys Phe			
105	110	115	
agc cgc cat cat gga ccc acc att act gcc aag ctc tac ggg cg ^g g ^c g ^c			725
Ser Arg His His Gly Pro Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala			
120	125	130	135
ccg cag ctg agg gaa act ctc ctg cag gac ttc aga gtg gtt gcc cag			773
Pro Gln Leu Arg Glu Thr Leu Leu Gln Asp Phe Arg Val Val Ala Gln			
140	145	150	
ggt gtg ggc atc cct gag gac tcc atc ttc acc atg gct gac cga ggt			821
Gly Val Gly Ile Pro Glu Asp Ser Ile Phe Thr Met Ala Asp Arg Gly			
155	160	165	
gaa tgt gtc cct ggg gag cag gaa cca gag ccc atc tta atc ccg aga			869
Glu Cys Val Pro Gly Glu Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg			
170	175	180	
gtc cgg agg gct gct acc cca aga aga gga agg atc agg ggg tgg gca			917
Val Arg Arg Ala Ala Thr Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala			
185	190	195	
act ggt aac tgaagtccacc aagaaagaag attcctgcc a gctggctac			966
Thr Gly Asn			
200			
tcggccggtc cctgcatgg aatgaccagc aggtatttct ataatggta atccatggcc			1026
tgtgagactt tccagtacgg cggtgcattg ggcaacggta acaacttcgt cacagaaaag			1086
gagtgtctgc agacctgccc aactgtggcg gcctgcaatc tccccatagt cggggcccc			1146
tgccgagct tcattccagct ctgggcattt gatgctgtca agggaaagtg cgtcctcttc			1206
ccctacgggg gctgccaggg caacgggaac aagttctact cagagaaggg gtgcagagag			1266
tactgcggtg tccctggta tggtgatgag gagctgctgc gcttctccaa ctgacaactg			1326
gccggcttcgc aagtccaggg atggccagtg tctgtcccg ggtcctgtgg caggcagcgc			1386
caagcaacct gggccaaat aaaaactaaa ttgcaaaaaa aaaaaaaaaa			1436

<210> 8
 <211> 221
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..19

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 Val Ser Ala Gly Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln
 1 5 10
 Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala
 15 20 25
 Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr
 30 35 40 45
 Val Ser Thr Leu Val Leu Gly Glu Ala Thr Glu Ala Glu Ile Ser

50	55	60
Met Thr Ser Thr Arg Trp Arg Lys	Gly Val Cys Glu Glu	Thr Ser Gly
65	70	75
Ala Tyr Glu Lys Thr Asp Thr Asp	Gly Lys Phe Leu Tyr	His Lys Ser
80	85	90
Lys Trp Asn Ile Thr Met Glu Ser	Tyr Val Val His	Thr Asn Tyr Asp
95	100	105
Glu Tyr Ala Ile Phe Leu Thr Lys	Lys Phe Ser Arg	His His Gly Pro
110	115	120
Thr Ile Thr Ala Lys Leu Tyr Gly	Arg Ala Pro Gln Leu Arg	Glu Thr
130	135	140
Leu Leu Gln Asp Phe Arg Val Val	Ala Gln Gly Val Gly	Ile Pro Glu
145	150	155
Asp Ser Ile Phe Thr Met Ala Asp	Arg Gly Glu Cys Val	Pro Gly Glu
160	165	170
Gln Glu Pro Glu Pro Ile Leu Ile	Pro Arg Val Arg Arg	Ala Ala Thr
175	180	185
Pro Arg Arg Gly Arg Ile Arg Gly	Trp Ala Thr Gly Asn	
190	195	200

<210> 9
 <211> 2132
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..92

<220>
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 <222> 93..551

<220>
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 <222> 552..2132

<220>
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 <222> 2085..2090

<220>
 <221> polyA_site
 <222> 2117..2132

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 ctggggctg gtctgcaggg ttgacctgcg ca atg cag agg ctg cag gta gtg 113
 Met Gln Arg Leu Gln Val Val
 -35 -30
 ctg ggc cac ctg agg ggt ccg gcc gat tcc ggc tgg atg ccg cag gcc 161
 Leu Gly His Leu Arg Gly Pro Ala Asp Ser Gly Trp Met Pro Gln Ala
 -25 -20 -15
 gcg cct tgc ctg agc ggt gcc ccg cag gcc tcg gcc gcg gac gtg gtg 209
 Ala Pro Cys Leu Ser Gly Ala Pro Gln Ala Ser Ala Ala Asp Val Val
 -10 -5 1

gtg	gtg	cac	ggg	cgg	cgc	acg	gcc	atc	tgc	cgg	gca	cgc	ggc	ggc	257
Val	Val	His	Gly	Arg	Arg	Thr	Ala	Ile	Cys	Arg	Ala	Gly	Arg	Gly	
5				10					15				20		
ttc	aag	gac	acc	acc	ccc	gac	gag	ctt	ctc	tcg	gca	gtc	atg	acc	305
Phe	Lys	Asp	Thr	Thr	Pro	Asp	Glu	Leu	Leu	Ser	Ala	Val	Met	Thr	Ala
				25					30				35		
gtt	ctc	aag	gac	gtg	aat	ctg	agg	ccg	gaa	cag	ctg	ggg	gac	atc	353
Val	Leu	Lys	Asp	Val	Asn	Leu	Arg	Pro	Glu	Gln	Leu	Gly	Asp	Ile	Cys
				40				45				50			
gtc	gga	aat	gtg	ctg	cag	cct	ggg	gcc	ggg	gca	atc	atg	gcc	cga	401
Val	Gly	Asn	Val	Leu	Gln	Pro	Gly	Ala	Gly	Ala	Ile	Met	Ala	Arg	Ile
				55				60				65			
gcc	cag	ttt	ctg	agt	gac	atc	ccg	gag	act	gtg	cct	ttg	tcc	act	449
Ala	Gln	Phe	Leu	Ser	Asp	Ile	Pro	Glu	Thr	Val	Pro	Leu	Ser	Thr	Val
				70			75				80				
aat	aga	cag	tgt	tcg	ggg	cta	cag	gca	gtg	gcc	agc	ata	gca	ggg	497
Asn	Arg	Gln	Cys	Ser	Ser	Gly	Leu	Gln	Ala	Val	Ala	Ser	Ile	Ala	Gly
				85			90				95			100	
tgg	agt	cca	tgt	ccc	tgg	ctg	aca	gag	gga	acc	ctg	gaa	ata	tta	545
Trp	Ser	Pro	Cys	Pro	Trp	Leu	Thr	Glu	Gly	Thr	Leu	Glu	Ile	Leu	Leu
				105			110				115				
cgc	gct	tgtatggagaa	ggagaaggcc	agagattgcc	tgattcctat	ggggataacc									601
Arg	Ala														
tctgagaatg	tggctgagcg	gtttggcatt	tcacgggaga	agcaggatac	ctttgccttg										661
gcttcccagc	agaaggcagc	aagagcccag	agcaagggct	gtttccaagc	tgagattgtg										721
cctgtgacca	ccacggtcca	tgtatgacaag	ggcaccaaga	ggagcatcac	tgtgacccag										781
gatgagggta	tccggccca	caccaccatg	gagggctgg	ccaaactgaa	gcctgccttc										841
aagaaaagatg	gttctaccac	agctggtgag	actggtccgg	ggtaggggta	tgagaaagca										901
ggccatggcc	atgctgggtg	ctgtactctg	ggaacctgga	atagaccagg	ccctctgca										961
aagtagaagt	gggagggctg	ggatctccctc	atccccaccc	cgatgccttc	ttaccccaac										1021
agtttgc	ccccc	taggaaactc	tagccaggtg	agtgtatgggg	cagctgccc	cctgctggcc									1081
cgagggtcca	aggcagaaga	gttgggcctt	cccatcctt	gggtcctgag	gtcttatgca										1141
gtggttgggg	tcccacctga	catcatggc	attggacctg	cctatgccc	cccagtagct										1201
ttgcaaaaag	caggtaaggt	ggctccttca	tatagtatct	gggtcccacc	tggatcctgc										1261
agctgc	catgctgttgc	ccaggggcat	gagggtggtc	ctgtgggtgc	tgcagagtgg										1321
aggtggggca	ggctagtg	ccatacttca	agcccttc	gacccca	ctgggatttgg										1381
ctcaccc	tggagagac	acacaccagg	cagcctgt	gccatggat	gggggtggcc										1441
ccaggggagg	cagagggcca	gtgtgtcagc	tcaggtctt	accttgtctg	caggcgtgac										1501
agtgagtgac	gtggacatct	tgcagatcaa	tgaggcctt	gcaagccagg	ctgcctactg										1561
tgtggagaag	ctacgactcc	cccctgagaa	ggtgaacccc	ctgggggggtg	cagtggcctt										1621
agggcacc	ctgggctgca	ctggggcaccg	acaggtc	acgctgtca	atgagctgaa										1681
gcccgtgg	aagagggcat	acggagtggt	gtccatgtgc	atcgggactg	gaatgggagc										1741
cgctggc	tttgaatacc	ctgggaactg	agtggaggtcc	caggctggag	gcccgtgg										1801
gacagtcc	ctgctctagc	agcaaggcag	taacaccaca	aaagcaaaac	cacatgggaa										1861
aactcagcac	tggtggtgt	ggcagtg	agatcaaggc	acttcaactc	atttggaaaa										1921
tgtgaacact	gatgacatgg	tataggagt	ggtgggtgt	tgagccaccc	atcagaccct										1981
ctttagctgt	gcaagataaa	agcagcctgg	gtcacc	ccacaaggcc	atggtaatt										2041
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ttatcttaaa	aaaagaaaaaa	aaaaaaa	a												2132

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 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> 1..35

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-35 -30 -25 -20
Ser Gly Trp Met Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln
-15 -10 -5
Ala Ser Ala Ala Asp Val Val Val His Gly Arg Arg Thr Ala Ile
1 5 10
Cys Arg Ala Gly Arg Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu
15 20 25
Leu Ser Ala Val Met Thr Ala Val Leu Lys Asp Val Asn Leu Arg Pro
30 35 40 45
Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala
50 55 60
Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp Ile Pro Glu
65 70 75
Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln
80 85 90
Ala Val Ala Ser Ile Ala Gly Trp Ser Pro Cys Pro Trp Leu Thr Glu
95 100 105
Gly Thr Leu Glu Ile Leu Leu Arg Ala
110 115

<210> 11
<211> 2266
<212> DNA
<213> Homo sapiens

<220>
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<222> 1..200

<220>
<221> CDS
<222> 201..986

<220>
<221> 3'UTR
<222> 987..2266

<220>
<221> polyA_signal
<222> 2233..2238

<220>
<221> polyA_site
<222> 2251..2266

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aaaaagaatc ctcatcatta atgcaagtgg aaggaaactc ttcacccaaag aattgtatcac 120
atcatgaaag gtgaaatcat tacggaattt cttaaatata taatttgaat ctggatttaa 180
aaataataaa tgtgatcagg atg ccc ttc tct cat ctg tct acc tac agc ctg 233
Met Pro Phe Ser His Leu Ser Thr Tyr Ser Leu

-20	-15	
gtt tgg gtc atg gca gca gtg gtg ctg tgc aca gca caa gtg caa gtg		281
Val Trp Val Met Ala Ala Val Val Leu Cys Thr Ala Gln Val Gln Val		
-10	-5	1
gtg acc cag gat gaa aga gag cag ctg tac aca act gct tcc tta aaa		329
Val Thr Gln Asp Glu Arg Glu Gln Leu Tyr Thr Thr Ala Ser Leu Lys		
5	10	15
tgc tct ctg caa aat gcc cag gaa gcc ctc att gtg aca tgg cag aaa		377
Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys		
25	30	35
aag aaa gct gta agc cca gaa aac atg gtc acc ttc agc gag aac cat		425
Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr Phe Ser Glu Asn His		
40	45	50
ggg gtg gtg atc cag cct gcc tat aag gac aag ata aac att acc cag		473
Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln		
55	60	65
ctg gga ctc caa aac tca acc atc acc ttc tgg aat atc acc ctg gag		521
Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu		
70	75	80
gat gaa ggg tgt tac atg tgt ctc aat acc ttt ggt ttt ggg aag		569
Asp Glu Gly Cys Tyr Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys		
85	90	95
atc tca gga acg gcc tgc ctc acc gtc tat gta cag ccc ata gta tcc		617
Ile Ser Gly Thr Ala Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser		
105	110	115
ctt cac tac aaa ttc tct gaa gac cac cta aat atc act tgc tct gcc		665
Leu His Tyr Lys Phe Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala		
120	125	130
act gcc cgc cca gcc ccc atg gtc ttc tgg aag gtc cct cgg tca ggg		713
Thr Ala Arg Pro Ala Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly		
135	140	145
att gaa aat agt aca gtg act ctg tct cac cca aat ggg acc acg tct		761
Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser		
150	155	160
gtt acc agc atc ctc cat atc aaa gac cct aag aat cag gtg ggg aag		809
Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys		
165	170	175
gag gtg atc tgc cag gtg ctg cac ctg ggg act gtg acc gac ttt aag		857
Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val Thr Asp Phe Lys		
185	190	195
caa acc gtc aac aaa ggc tat tgg ttt tca gtt ccg cta ttg cta agc		905
Gln Thr Val Asn Lys Gly Tyr Trp Phe Ser Val Pro Leu Leu Ser		
200	205	210
att gtt tcc ctg gta att ctt ctc gtc cta atc tca atc tta ctg tac		953
Ile Val Ser Leu Val Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr		
215	220	225
tgg aaa cgt cac cgg aat cag gac cga gag ccc taaataagtc acacagcacc	1006	
Trp Lys Arg His Arg Asn Gln Asp Arg Glu Pro		
230	235	
ctgaaaagtga ttccctggtc tacttgaatt tgacacaaga gaaaaggcagg agaaaaaggg	1066	
gccattctcc aaaggacctg aaagagcaaa agagggtggaa gcgaaagcct taaggatccc	1126	
acgacttttt actgccatct gagctactca gtgttgaat cccaaaggaga agtcagttt	1186	
cctctcaggt ctgtttagg acttgattt gtaaagcaat gccatgttat gtgggtgaaa	1246	
gggcactgga cttagttagt atcaggagca ctgagctcac agactgactt gggctctac	1306	
tggtggggac ctctgttagt cacttacct catccaaagt ataaaggaat tggaccaaat	1366	
aatttaccac atagctctaa aacttaattt aaaatgtaat tccagaaaaaaa aaaaggaaat	1426	

aagcaaaggg	ggaagaattt	aaagagagag	agaagaaaaga	atacagagag	cttacctttt	1486
gccttctgt	tgtatgttaca	tctcttcttc	ctatgttctt	aggcttatga	gtctgttcc	1546
ccatcatttgc	gtatctagtc	cagttcctgc	ttactgctt	gctaatacg	ggccttgcta	1606
gaatccttgg	tttcaactgct	gttcttcatg	tgcttctatg	agatttactc	caacacaaaat	1666
aggactgaat	ttattgtgaa	gtaacattgg	caatcttaac	ttattcattt	aacttatttt	1726
tatacgat	taaatattgt	tagtctttaga	caatagctca	catttttga	gaagcatgcc	1786
ctccctgtcc	atttgtctta	taacatgacc	cagccctatt	ttacgtcatt	ctaaattcag	1846
cctcatataa	tgaaaatacata	ttatgaaaac	agatgtttag	gagatttct	gtatagcagt	1906
cagccaattt	atatgcttttgc	tctctgttgg	cttctttttc	catcgctta	ctttcccaa	1966
tagcagagga	ggcaaatatgc	agcataacaat	ccctttgttc	taaagatatt	gttccagcta	2026
gtggaatgtat	gttgaatctt	taataaccat	aatttagttgc	tttttcagta	tcttctgttt	2086
tgtctgtgtc	tatccagtgg	ccttagaattt	aaagtgttaag	ttgtttcgc	tgtaaatttg	2146
gatatttata	tatatatata	tagcaagattt	tcatgtgtt	atthaattct	gtattgtttc	2206
ttatatttgt	agtaaaaatata	tgaacaattt	aaagtgttga	ctccaaaaaa	aaaaaaaaaa	2266

<210> 12

<211> 262

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..23

<400> 12

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 -20 -15 -10

Ala Val Val Leu Cys Thr Ala Gln Val Gln Val Val Thr Gln Asp Glu
-5 1 5

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Pro Glu Asn Met Val Thr Phe Ser Glu Asn His Gly Val Val Ile Gln
45 50 55

Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln Leu Gly Leu Gln Asn
 60 65 70

Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu Asp Glu Gly Cys Tyr
75 80 85

Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys Ile Ser Gly Thr Ala
90 95 100 105

Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser Leu His Tyr Lys Phe
 110 115 120

Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala Thr Ala Arg Pro Ala
125 130 135

Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly Ile Glu Asn Ser Thr
140 145 150

Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser Val Thr Ser Ile Leu
155 160 165

His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys Glu Val Ile Cys Gln
170 175 180 185

Val Leu His Leu Gly Thr Val Thr Asp Phe Lys Gln Thr Val Asn Lys
 190 195 200

Gly Tyr Trp Phe Ser Val Pro Leu Leu Leu Ser Ile Val Ser Leu Val
 205 210 215

Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr Trp Lys Arg His Arg

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Met	Glu	Arg	Met	Leu	Pro	Leu	Leu	Thr	Leu	Gly	Leu	Leu	Ala	Ala		
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Gly	Phe	Cys	Pro	Ala	Val	Leu	Cys	His	Pro	Asn	Ser	Pro	Leu	Asp	Glu	
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Glu	Asn	Leu	Thr	Gln	Glu	Asn	Gln	Asp	Arg	Gly	Thr	His	Val	Asp	Leu	
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Gly	Leu	Ala	Ser	Ala	Asn	Val	Asp	Phe	Ala	Leu	Ser	Leu	Tyr	Lys	Gln	
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tta	gtc	ctg	aag	gcc	cct	gat	aag	aat	gtc	atc	ttc	tcc	cca	ctg	agc	302
Leu	Val	Leu	Lys	Ala	Pro	Asp	Lys	Asn	Val	Ile	Phe	Ser	Pro	Leu	Ser	
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Ile	Ser	Thr	Ala	Leu	Ala	Phe	Leu	Ser	Leu	Gly	Ala	His	Asn	Thr	Thr	
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ctg	aca	gag	att	ctc	aaa	ggc	ctc	aag	ttc	aac	ctc	acg	gag	act	tct	398
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Leu	Lys	Phe	Asn	Leu	Thr	Glu	Thr	Ser	
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Glu	Ala	Glu	Ile	His	Gln	Ser	Phe	Gln	His	Leu	Leu	Arg	Thr	Leu	Asn	
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cag	tcc	agc	gat	gag	ctg	cag	ctg	agt	atg	gga	aat	gcc	atg	ttt	gtc	494

Gln	Ser	Ser	Asp	Glu	Leu	Gln	Leu	Ser	Met	Gly	Asn	Ala	Met	Phe	Val	
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Lys	Glu	Gln	Leu	Ser	Leu	Leu	Asp	Arg	Phe	Thr	Glu	Asp	Ala	Lys	Arg	
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ctg	tat	ggc	tcc	gag	gcc	ttt	gcc	act	gac	ttt	cag	gac	tca	gct	gca	590
Leu	Tyr	Gly	Ser	Glu	Ala	Phe	Ala	Thr	Asp	Phe	Gln	Asp	Ser	Ala	Ala	
				140				145					150			
gct	aag	aag	ctc	atc	aac	gac	tac	gtg	aag	aat	gga	act	agg	ggg	aaa	638
Ala	Lys	Leu	Ile	Asn	Asp	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Gly	Lys		
				155				160					165			
atc	aca	gat	ctg	atc	aag	gac	ctt	gac	tcg	cag	aca	atg	atg	gtc	ctg	686
Ile	Thr	Asp	Leu	Ile	Lys	Asp	Leu	Asp	Ser	Gln	Thr	Met	Met	Val	Leu	
				170				175					180			
gtg	aat	tac	atc	tcc	ttt	aaa	gcc	aaa	tgg	gag	atg	ccc	ttt	gac	ccc	734
Val	Asn	Tyr	Ile	Phe	Phe	Lys	Ala	Lys	Trp	Glu	Met	Pro	Phe	Asp	Pro	
				185				190					195		200	
caa	gat	act	cat	cag	tca	agg	tcc	tac	ttg	agc	aag	aaa	aag	tgg	gta	782
Gln	Asp	Thr	His	Gln	Ser	Arg	Phe	Tyr	Leu	Ser	Lys	Lys	Trp	Val		
				205				210					215			
atg	gtg	ccc	atg	atg	agt	ttg	cat	cac	ctg	act	ata	cct	tac	ttc	cg	830
Met	Val	Pro	Met	Met	Ser	Leu	His	His	Leu	Thr	Ile	Pro	Tyr	Phe	Arg	
				220				225					230			
gac	gag	gag	ctg	tcc	tgc	acc	gtg	gtg	gag	ctg	aag	tac	aca	ggc	aat	878
Asp	Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	Tyr	Thr	Gly	Asn	
				235				240					245			
gcc	agc	gca	ctc	tcc	atc	ctc	cct	gat	caa	gac	aag	atg	gag	gaa	gtg	926
Ala	Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	Met	Glu	Glu	Val	
				250				255					260			
gaa	gcc	atg	ctg	ctc	cca	gag	acc	ctg	aag	cg	tgg	aga	gac	tct	ctg	974
Glu	Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	Arg	Asp	Ser	Leu	
				265				270					275		280	
gag	ttc	aga	gag	ata	ggt	gag	ctc	tac	ctg	cca	aag	ttt	tcc	atc	tcg	1022
Glu	Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Ser	
				285				290					295			
agg	gac	tat	aac	ctg	aac	gac	ata	ctt	ctc	cag	ctg	ggc	att	gag	gaa	1070
Arg	Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Leu	Gln	Leu	Gly	Ile	Glu	Glu	
				300				305					310			
gcc	tcc	acc	agc	aag	gct	gac	ctg	tca	ggg	atc	aca	ggg	gcc	agg	aac	1118
Ala	Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	Gly	Ala	Arg	Asn	
				315				320					325			
cta	gca	gtc	tcc	cag	gtg	gtc	cat	aag	gct	gt	ctt	gat	gta	ttt	gag	1166
Leu	Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	Asp	Val	Phe	Glu	
				330				335					340			
gag	ggc	aca	gaa	gca	tct	gct	gcc	aca	gca	gtc	aaa	atc	acc	ctc	ctt	1214
Glu	Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	Ile	Thr	Leu	Leu	
				345				350					355		360	
tct	gca	tta	gtg	gag	aca	agg	acc	att	gtg	cgt	ttc	aac	agg	ccc	ttc	1262
Ser	Ala	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	Asn	Arg	Pro	Phe	
				365				370					375			
ctg	atg	atc	att	gtc	cct	aca	gac	acc	cag	aac	atc	ttc	ttc	atg	agc	1310
Leu	Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile	Phe	Phe	Met	Ser	
				380				385					390			
aaa	gtc	acc	aat	ccc	aag	caa	gcc	tagagcttgc	catcaaggcag	tggggctctc						1364
Lys	Val	Thr	Asn	Pro	Lys	Gln	Ala									
				395				400								

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 tccctgtgt a gctctcacat gcacaggggc ccatggactc ttcagtctgg agggtcctgg 1544
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 Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln Leu
 30 35 40
 Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile
 45 50 55
 Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu
 60 65 70
 Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu
 75 80 85
 Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn Gln
 90 95 100 105
 Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys
 110 115 120
 Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu
 125 130 135
 Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala
 140 145 150
 Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile
 155 160 165
 Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu Val
 170 175 180 185
 Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln
 190 195 200
 Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Trp Val Met
 205 210 215
 Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp
 220 225 230
 Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala
 235 240 245
 Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu
 250 255 260 265
 Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu
 270 275 280
 Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg
 285 290 295
 Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala

300	305	310	
Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu			
315	320	325	
Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu Glu			
330	335	340	345
Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser			
350	355	360	
Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu			
365	370	375	
Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys			
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Val Thr Asn Pro Lys Gln Ala			
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Met Gly Ser Ala Ala Leu Glu			
1	5		
atc ctg ggc ctg gtg ctg tgc ctg gtg ggc tgg ggg ggt ctg atc ctg			221
Ile Leu Gly Leu Val Leu Cys Leu Val Gly Trp Gly Gly Leu Ile Leu			
10	15	20	
gcg tgc ggg ctg ccc atg tgg cag gtg acc gcc ttc ctg gac cac aac			269
Ala Cys Gly Leu Pro Met Trp Gln Val Thr Ala Phe Leu Asp His Asn			
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atc gtg acg gcg cag acc acc tgg aag ggg ctg tgg atg tcg tgc gtg			317
Ile Val Thr Ala Gln Thr Trp Lys Gly Leu Trp Met Ser Cys Val			
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Val Gln Ser Thr Gly His Met Gln Cys Lys Val Tyr Asp Ser Val Leu			
365			

60	65	70		
gct ctg agc acc gag gtg cag gcg gcg cg	ctc acc gtg agc gcc		413	
Ala Leu Ser Thr Glu Val Gln Ala Ala Arg Ala	Leu Thr Val Ser Ala			
75	80	85		
gtg ctg ctg gcg ttc gtt gcg ctc ttc gtg acc	ctg gcg ggc gcg cag		461	
Val Leu Leu Ala Phe Val Ala Leu Phe Val Thr	Leu Ala Gly Ala Gln			
90	95	100		
tgc acc acc tgc gtg gcc ccg ggc ccg gcc aag	gcg cgt gtg gcc ctc		509	
Cys Thr Thr Cys Val Ala Pro Gly Pro Ala Lys	Ala Arg Val Ala Leu			
105	110	115		
acg gga ggc gtg ctc tac ctg ttt tgc ggg ctg	ctg gcg ctc gtg cca		557	
Thr Gly Gly Val Leu Tyr Leu Phe Cys Gly	Leu Leu Ala Leu Val Pro			
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ctc tgc tgg ttc gcc aac att gtc gtc cgc gag	ttt tac gac ccg tct		605	
Leu Cys Trp Phe Ala Asn Ile Val Val Arg	Glu Phe Tyr Asp Pro Ser			
140	145	150		
gtg ccc gtg tcg cag aag tac gag ctg ggc gca	gcg ctg tac atc ggc		653	
Val Pro Val Ser Gln Lys Tyr Glu Leu Gly	Ala Ala Leu Tyr Ile Gly			
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tgg gcg gcc acc gcg ctg ctc atg gta ggc ggc	tcg ctc ttg tgc tgc		701	
Trp Ala Ala Thr Ala Leu Leu Met Val Gly	Gly Cys Leu Leu Cys Cys			
170	175	180		
ggc gcc tgg gtc tgc acc ggc cgt ccc gac ctc	agc ttc ccc gtg aag		749	
Gly Ala Trp Val Cys Thr Gly Arg Pro Asp	Leu Ser Phe Pro Val Lys			
185	190	195		
tac tca gcg ccg cgg ccc acg gcc acc ggc	gac aac gac aag aag		797	
Tyr Ser Ala Pro Arg Arg Pro Thr Ala Thr	Gly Asp Asn Asp Lys			
200	205	210	215	
aac tac gtc tgagggcgct gggcacggcc	gggccccctcc tgccagccac		846	
Asn Tyr Val				
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gcgcggcgcg caggcttctc ggaacgtccg	gctctgcgcc ccgcacgcggc tcctggatcc		966	
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 Thr Ala Phe Leu Asp His Asn Ile Val Thr Ala Gln Thr Thr Trp Lys
 35 40 45
 Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly His Met Gln Cys
 50 55 60
 Lys Val Tyr Asp Ser Val Leu Ala Leu Ser Thr Glu Val Gln Ala Ala

65	70	75	80
Arg Ala Leu Thr Val Ser Ala Val Leu Leu Ala Phe Val Ala Leu Phe			
85	90	95	
Val Thr Leu Ala Gly Ala Gln Cys Thr Thr Cys Val Ala Pro Gly Pro			
100	105	110	
Ala Lys Ala Arg Val Ala Leu Thr Gly Gly Val Leu Tyr Leu Phe Cys			
115	120	125	
Gly Leu Leu Ala Leu Val Pro Leu Cys Trp Phe Ala Asn Ile Val Val			
130	135	140	
Arg Glu Phe Tyr Asp Pro Ser Val Pro Val Ser Gln Lys Tyr Glu Leu			
145	150	155	160
Gly Ala Ala Leu Tyr Ile Gly Trp Ala Ala Thr Ala Leu Leu Met Val			
165	170	175	
Gly Gly Cys Leu Leu Cys Cys Gly Ala Trp Val Cys Thr Gly Arg Pro			
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Asp Leu Ser Phe Pro Val Lys Tyr Ser Ala Pro Arg Arg Pro Thr Ala			
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Thr Gly Asp Asn Asp Lys Lys Asn Tyr Val			
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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
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gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45

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Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu	
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Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro	
65 70 75	
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Leu Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val	
80 85 90 95	
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Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu	
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ctg ctg tat ggg ctg gtg agc aca gca ctg atc tgg cat ccc atc	443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile	
115 120 125	
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc	491
Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr	
130 135 140	
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca	539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro	
145 150 155	
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Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp	
160 165 170	
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caccckaatg ggaccacccct cctgggtccc ctggccgt ttttccttag aaatcagaga	712
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50 55 60	
Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu	
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Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu	
85 90 95	
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu His Leu Leu Leu	
100 105 110	
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn	
115 120 125	
Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val	
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His Gln Pro Gln Pro Thr Glu Lys Ser Asp	

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170

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 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt ttg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140

gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggagggac gcccagggtg gggaggaaga gtctgcaagc agggctgtgg agttagggtt 652
 caccccaatg ggaccaccct cctgggtccc ctgggccgt tttccttag aaatcagaga 712
 aatggaaag gggggaaac tgattttaca cttaaataat aaaatcctat tagtaactct 772
 caaaaaaaaaaaaaaaa 789

<210> 20
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 20
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 1 5 10 15
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 21
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 <212> DNA
 <213> Homo sapiens

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 <222> 86..403

<220>
 <221> 3'UTR
 <222> 404..555

<220>
 <221> polyA_signal
 <222> 504..509

<220>
 <221> polyA_site
 <222> 540..555

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 agagtcaagg gcacgagcat cggcc atg cct ttc ttg gac atc cag aaa agg 112
 Met Pro Phe Leu Asp Ile Gln Lys Arg
 1 5

ttc ggc ctt aac ata gat cga tgg ttg aca atc cag agt tgt gaa cag 160
 Phe Gly Leu Asn Ile Asp Arg Trp Leu Thr Ile Gln Ser Cys Glu Gln
 10 15 20 25

ccc tac aag atg gct ggt cga tgc cat gct ttt gaa aaa gaa tgg ata 208
 Pro Tyr Lys Met Ala Gly Arg Cys His Ala Phe Glu Lys Glu Trp Ile
 30 35 40

gaa tgt gca cat gga atc ggt tat act cgg gca gag aaa gag tgc aag 256
 Glu Cys Ala His Gly Ile Gly Tyr Thr Arg Ala Glu Lys Glu Cys Lys
 45 50 55

ata gaa tat gat gat ttc gta gag tgt ttg ctt cgg cag aaa acg atg 304
 Ile Glu Tyr Asp Asp Phe Val Glu Cys Leu Leu Arg Gln Lys Thr Met
 60 65 70

aga cgt gca ggt acc atc agg aag cag cgg gat aag ctg ata aag gaa 352
 Arg Arg Ala Gly Thr Ile Arg Lys Gln Arg Asp Lys Leu Ile Lys Glu
 75 80 85

gga aag tac acc cct cca cct cac cac att ggc aag ggg gag cct tgg 400
 Gly Lys Tyr Thr Pro Pro His His Ile Gly Lys Glu Pro Trp
 90 95 100 105

ccc tgaacagagc agctgctgat gtctggaggc tgatttcct gttctctgtt 453
 Pro

ctccactgga aaggttgttt acgacaaacc tccttgc当地 agtgtgtaaa aataaaggat 513
 tgctccatcc tatttgc当地 atttcaaaa aaaaaaaaaa aa 555

<210> 22
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 22
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Trp Leu Thr Ile Gln Ser Cys Glu Gln Pro Tyr Lys Met Ala Gly Arg
 20 25 30

Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly Ile Gly
 35 40 45

Tyr Thr Arg Ala Glu Lys Glu Cys Lys Ile Glu Tyr Asp Asp Phe Val
 50 55 60

Glu Cys Leu Leu Arg Gln Lys Thr Met Arg Arg Ala Gly Thr Ile Arg
 65 70 75 80

Lys Gln Arg Asp Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro Pro Pro
 85 90 95

His His Ile Gly Lys Glu Pro Trp Pro

100 105

<210> 23
 <211> 1726
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..414

<220>
 <221> CDS
 <222> 415..1653

<220>
 <221> 3'UTR
 <222> 1654..1726

<220>
 <221> polyA_site
 <222> 1688..1726

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 cgcgtcgggt ggggcgggaa taaagttttt ccaaccagt ttggggagag ggctggatgg 180
 gaaggaccct ccctgctgca gacttcatgg caggctgcac tgtgtccct cggctccacg 240
 gctgccccgg gggcgctgct ttccgggtttt ctttcttagaa tctctggctct gctgctgtgc 300
 agatggacct gccggcaactg ctgtcagaag tgctacgagt ccagctgttg ccagtcaagt 360
 gaggatgaag ttgaaattct gggaccttcc cctgctcaga cccctccctg gctg atg 417
 Met
 1
 gcc agc cgg agc agt gac aag gat ggt gac tct gtc cac acg gcc agc 465
 Ala Ser Arg Ser Ser Asp Lys Asp Gly Asp Ser Val His Thr Ala Ser
 5 10 15
 gaa gtc ccg ctg acc cca cgg acc aat tcc ccg gat gga aga cgc tcg 513
 Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg Ser
 20 25 30
 tcc tca gac aca tcc aag tct aca tac agc ctg acg cgg agg att tcg 561
 Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser
 35 40 45
 agt ctt gag tca aga cgt ccc agc tct cca ctc atc gat att aaa ccc 609
 Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro
 50 55 60 65
 atc gag ttt ggc gtt ctc agc gcc aag aag gag ccc atc caa cct tcg 657
 Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro Ser
 70 75 80
 gtg ctc aga cgg acc tat aac ccc gac gac tat ttc agg aag ttc gaa 705
 Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe Glu
 85 90 95
 ccc cac ctg tac tcc ctc gac tcc aac agc gac gat gtg gac tct ctg 753
 Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser Leu
 100 105 110
 aca gac gag gag atc ctg tcc aag tac cag ctg ggc atg cag cac ttc 801
 Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His Phe

115	120	125	
agc act cag tac gac ctg ctg cac aac cac ctc acc gtg cgc gtg atc			849
Ser Thr Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val Ile			
130	135	140	145
gag gcc agg gac ctg cca cct ccc atc tcc cac gat ggc tcg cgc cag			897
Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg Gln			
150	155	160	
gac atg gcg cac tcc aac ccc tac gtc aag atc tgt ctc ctg cca gac			945
Asp Met Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro Asp			
165	170	175	
cag aag aac tca aag cag acc ggg gtc aaa cgc aag acc cag aag ccc			993
Gln Lys Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys Pro			
180	185	190	
gtg ttt gag gag cgc tac acc ttc gag atc ccc ttc ctg gag gcc cag			1041
Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala Gln			
195	200	205	
agg agg acc ctg ctc ctg acc gtg gtg gat ttt gat aag ttc tcc cgc			1089
Arg Arg Thr Leu Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser Arg			
210	215	220	225
cac tgt gtc att ggg aaa gtt tct gtg cct ttg tgt gaa gtt gac ctg			1137
His Cys Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp Leu			
230	235	240	
gtc aag ggc ggg cac tgg tgg aag gcg ctg att ccc agt tct cag aat			1185
Val Lys Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln Asn			
245	250	255	
gaa gtg gag ctg ggg gag ctg ctt ctg tca ctg aat tat ctc cca agt			1233
Glu Val Glu Leu Gly Glu Leu Leu Ser Leu Asn Tyr Leu Pro Ser			
260	265	270	
gct ggc aga ctg aat gtt gat gtc att cga gcc aag caa ctt ctt cag			1281
Ala Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln			
275	280	285	
aca gat gtg agc caa ggt tca gac ccc ttt gtg aaa atc cag ctg gtg			1329
Thr Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val			
290	295	300	305
cat gga ctc aaa ctt gtg aaa acc aag aag acg tcc ttc tta agg ggc			1377
His Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly			
310	315	320	
aca att gat cct ttc tac aat gaa tcc ttc agc ttc aaa gtt ccc caa			1425
Thr Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln			
325	330	335	
gaa gaa ctg gaa aat gcc agc cta gtg ttt aca gtt ttc ggc cac aac			1473
Glu Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn			
340	345	350	
atg aag agc agc aat gac ttc atc ggg agg atc gtc att ggc cag tac			1521
Met Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr			
355	360	365	
tct tca ggc ccc tct gag acc aac cac tgg agg cgc atg ctc aac acg			1569
Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr			
370	375	380	385
cac cgc aca gcc gtg gag cag tgg cat agc ctg agg tcc cga gct gag			1617
His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala Glu			
390	395	400	
tgt gac cgc gtg tct cct gcc tcc ctg gag gtg acc tgaggctgc			1663
Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr			
405	410		
agggaggca gctttcattt gttaaaaaaaaa aaaaaaaaaaa aaagacgaaa aaaaaaaaaa 1723			

aaa

1726

<210> 24
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 24
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 Ser Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg
 20 25 30
 Ser Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile
 35 40 45
 Ser Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys
 50 55 60
 Pro Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro
 65 70 75 80
 Ser Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe
 85 90 95
 Glu Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser
 100 105 110
 Leu Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His
 115 120 125
 Phe Ser Thr Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val
 130 135 140
 Ile Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg
 145 150 155 160
 Gln Asp Met Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro
 165 170 175
 Asp Gln Lys Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys
 180 185 190
 Pro Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala
 195 200 205
 Gln Arg Arg Thr Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser
 210 215 220
 Arg His Cys Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp
 225 230 235 240
 Leu Val Lys Gly Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln
 245 250 255
 Asn Glu Val Glu Leu Gly Glu Leu Leu Ser Leu Asn Tyr Leu Pro
 260 265 270
 Ser Ala Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu
 275 280 285
 Gln Thr Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu
 290 295 300
 Val His Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg
 305 310 315 320
 Gly Thr Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro
 325 330 335
 Gln Glu Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His
 340 345 350
 Asn Met Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln
 355 360 365
 Tyr Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn
 370 375 380

Thr His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala
 385 390 395 400
 Glu Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr
 405 410

<210> 25
 <211> 941
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
 <221> CDS
 <222> 76..339

<220>
 <221> 3'UTR
 <222> 340..941

<220>
 <221> polyA_signal
 <222> 903..908

<220>
 <221> polyA_site
 <222> 926..941

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 ccgaccctt gcacc atg gac ccc gct cgc ccc ctg ggg ctg tcg att ctg 111
 Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu
 -20 -15
 ctg ctt ttc ctg acg gag gct gca ctg ggc gat gct gct cag gag cca 159
 Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro
 -10 -5 1
 aca gga aat aac gcg gag atc tgt ctc ctg ccc cta gac tac gga ccc 207
 Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro
 5 10 15 20
 tgc cgg gcc cta ctt ctc cgt tac tac tac gac agg tac acg cag agc 255
 Cys Arg Ala Leu Leu Arg Tyr Tyr Asp Arg Tyr Thr Gln Ser
 25 30 35
 tgc cgc cag ttc ctg tac ggg ggc tgc gag ggc aac gcc aac aat ttc 303
 Cys Arg Gln Phe Leu Tyr Gly Cys Glu Gly Asn Ala Asn Asn Phe
 40 45 50
 tac acc tgg gag gct tgc gac gat ctt gct gga gga tagaaaaagt 349
 Tyr Thr Trp Glu Ala Cys Asp Asp Leu Ala Gly Gly
 55 60

tcccaaagtt tgccggctgc aagttagtgc ggacgaccag tggagggtt ccacagaaaa 409
 gtatccctt aatctaagtt ccatgacatg tgaaaaattc tttccgggtg ggtgtcaccg 469
 gaaccggatt gagaacaggt ttccagatga agctacttgt atgggcttct ggcacccaa 529
 gaaaattcca tcatccatgc acatccaaa agatggggac tggctctgc caatgtgact 589
 cgctattatt ttaatccaaat atacagaacc tggatgtcatt tcacccatac tggctgtgga 649
 gggatgaca ataacttgc tagcagggag gattgcaaac gtgcgtgc aaaagcttg 709

aaaaagaaaaa agaagatgcc aaagcttcgc tttgccagta gaatccggaa aattcggaaag 769
 aagcaatttt aaacatttctt aatatgtcat cttgttgctc ttatggctt atttgccttt 829
 atggttgtat ctgaagaata atatgacagc atgaggaaac aaatcattgg tgatttattc 889
 accagttttt attaatacaa gtcactttt aaaaataaaaa aaaaaaaaaaa aa 941

<210> 26
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 26
 Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
 -20 -15 -10
 Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
 -5 1 5
 Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
 10 15 20
 Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
 25 30 35 40
 Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
 45 50 55
 Ala Cys Asp Asp Leu Ala Gly Gly
 60

<210> 27
 <211> 1894
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..20

<220>
 <221> CDS
 <222> 21..1118

<220>
 <221> 3'UTR
 <222> 1119..1894

<220>
 <221> polyA_signal
 <222> 1858..1863

<220>
 <221> polyA_site
 <222> 1879..1894

<400> 27
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 Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala

-20	-15	
ctg gct ctt ctt tca gcg ttt tcg gcc acc cag gca cgg aaa ggc ttc		101
Leu Ala Leu Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe		
-10	-5	1
tgg gac tac ttc agc cag acc agc ggg gac aaa ggc agg gtg gag cag		149
Trp Asp Tyr Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln		
5	10	15
atc cat cag cag aag atg gct cgc gag ccc gcg acc ctg aaa gac agc		197
Ile His Gln Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser		
25	30	35
ctt gag caa gac ctc aac aat atg aac aag ttc ctg gaa aag ctg agg		245
Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg		
40	45	50
cct ctg agt ggg agc gag gct cct cgg ctc cca cag gac ccc gtg ggc		293
Pro Leu Ser Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly		
55	60	65
atg cgg cgg cag ctg cag gag gag ttg gag gag gtg aag gct cgc ctc		341
Met Arg Arg Gln Leu Gln Glu Leu Glu Leu Glu Val Lys Ala Arg Leu		
70	75	80
cag ccc tac atg gca gag gcg cac gag ctg gtg ggc tgg aat ttg gag		389
Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu		
85	90	95
ggc ttg cgg cag caa ctg aag ccc tac acg atg gat ctg atg gag cag		437
Gly Leu Arg Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln		
105	110	115
gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg		485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly		
120	125	130
gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct		533
Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala		
135	140	145
ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc		581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe		
150	155	160
aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg		629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly		
165	170	175
cgc cac gtg cag gag ctg cac cgc agt gtg gct ccg cac gcc ccc gcc		677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala		
185	190	195
agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc ccg aag ctc		725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu		
200	205	210
acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac		773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp		
215	220	225
cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag		821
Gln Leu Arg Glu Glu Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu		
230	235	240
gaa ggg gcc ggc ccg gac ccc cag atg ctc tcc gag gag gtg cgc cag		869
Glu Gly Ala Gly Pro Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln		
245	250	255
cga ctt cag gct ttc cgc cag gac acc tac ctg cag ata gct gcc ttc		917
Arg Leu Gln Ala Phe Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe		
265	270	275
act cgc gcc atc gac cag gag act gag gag gtc cag cag ctg gcg		965

Thr Arg Ala Ile Asp Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala			
280	285	290	
cca cct cca cca ggc cac agt gcc ttc gcc cca gag ttt caa caa aca			1013
Pro Pro Pro Pro Gly His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr			
295	300	305	
gac agt ggc aag gtt ctg agc aag ctg cag gcc cgt ctg gat gac ctg			1061
Asp Ser Gly Lys Val Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu			
310	315	320	
tgg gaa gac atc act cac agc ctt cat gac cag ggc cac agc cat ctg			1109
Trp Glu Asp Ile Thr His Ser Leu His Asp Gln Gly His Ser His Leu			
325	330	335	340
ggg gac ccc tgaggatcta cctggccagg cccattccca gcttcttgtc			1158
Gly Asp Pro			
tggggagcct tggctctgag cctctagcat gttcagttcc ttgaaagtgg cctgttgggt			1218
ggaggggtgga aggtcctgtg caggacaggg aggccaccaa agggctgtct gtctcctgca			1278
tatccagcct cctgcgactc cccaatctgg atgcattaca ttcaccaggc tttgcaaacc			1338
cagcctccca gtgctcattt gggaaatgctc atgagttact ccattcaagg gtgagggagt			1398
agggagggag aggcaccatg catgtgggtg attatctgca agcctgttg ccgtgatgt			1458
ggaagcctgt gccactacat cctggagttt ggctctagtc acttctggct gcctgggtgc			1518
cactgctaca gctggtccac agagaggagc acttgtctcc ccagggtctgc catggcagct			1578
atcaggggaa tagaagggag aaagagaata tcatggggag aacatgtat ggtgtgtgaa			1638
tatccctgct ggctctgtat ctgggtggta cgaaagggtt gggctgtat aggagagggc			1698
agagcccatg tttcctgaca tagctctaca cctaaataag ggactgaacc ctcccaactg			1758
tgggagctcc ttaaaccctc tggggagcat actgtgtgtct ctccccatct ccagccctc			1818
cctctgggtt cccaagttga agcctagact tctggctcaa atgaaataga tgtttatgtat			1878
aaaaaaaaaaaa aaaaaaaaaaaaa			1894

<210> 28
<211> 366
<212> PRT
<213> *Homo sapiens*

<220>
<221> SIGNAL
<222> 1..23

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<400> 28
Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser
-20 -15 -10
Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser
-5 1 5
Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys
10 15 20 25
Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu
30 35 40
Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser
45 50 55
Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu
60 65 70
Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala
75 80 85
Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln
90 95 100 105
Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val
110 115 120
Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala

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125	130	135
Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu		
140	145	150
Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His		
155	160	165
Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu		
170	175	180
Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu		
190	195	200
Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys		
205	210	215
Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu		
220	225	230
Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro		
235	240	245
Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe		
250	255	260
Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp		
270	275	280
Gln Glu Thr Glu Glu Val Gln Gln Leu Ala Pro Pro Pro Pro Gly		
285	290	295
His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val		
300	305	310
Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr		
315	320	325
His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro		
330	335	340

<210> 29
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..31

<220>
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<220>
 <221> 3'UTR
 <222> 560..742

<220>
 <221> polyA_signal
 <222> 702..707

<220>
 <221> polyA_site
 <222> 728..742

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 Met Thr Ser Gly Ser Lys Cys

1	5	
cct agt aca gac tca gga aaa gaa gaa tat att gcc acg ttc aaa gga		100
Pro Ser Thr Asp Ser Gly Lys Glu Glu Tyr Ile Ala Thr Phe Lys Gly		
10 15 20		
tct gaa tac ttc tgc tac gac ttg tct caa aac ccc att caa agc agc		148
Ser Glu Tyr Phe Cys Tyr Asp Leu Ser Gln Asn Pro Ile Gln Ser Ser		
25 30 35		
agt gat gaa ata act ctg tca ttt aaa acc ctt cag agg aat gga ctg		196
Ser Asp Glu Ile Thr Leu Ser Phe Lys Thr Leu Gln Arg Asn Gly Leu		
40 45 50 55		
atg ctt cac act ggg aaa tcg gct gat tat gtc aat ctt gcc ctg aaa		244
Met Leu His Thr Gly Lys Ser Ala Asp Tyr Val Asn Leu Ala Leu Lys		
60 65 70		
aat gga gct gtc tct ctg gtc att aat ttg gga tca ggg gcc ttt gaa		292
Asn Gly Ala Val Ser Leu Val Ile Asn Leu Gly Ser Gly Ala Phe Glu		
75 80 85		
gca cta gtg gag cct gtg aat gga aag ttt aat gat aat gcc tgg cat		340
Ala Leu Val Glu Pro Val Asn Gly Lys Phe Asn Asp Asn Ala Trp His		
90 95 100		
gat gtg aaa gtc acc agg aat ctg cgt cag gtg aca ata tca gtg gat		388
Asp Val Lys Val Thr Arg Asn Leu Arg Gln Val Thr Ile Ser Val Asp		
105 110 115		
ggg att ctt acc aca acg ggc tac acg caa gaa gat tat acc atg ctg		436
Gly Ile Leu Thr Thr Gly Tyr Thr Gln Glu Asp Tyr Thr Met Leu		
120 125 130 135		
ggg tct gat gac ttt ttc tat gtt gga ggc agt ccc agc aca gcc gac		484
Gly Ser Asp Asp Phe Phe Tyr Val Gly Gly Ser Pro Ser Thr Ala Asp		
140 145 150		
ctt cca ggg tca cca atc cag cat gaa agc acc ttt gct gaa gac ccg		532
Leu Pro Gly Ser Pro Ile Gln His Glu Ser Thr Phe Ala Glu Asp Pro		
155 160 165		
atg ttc cag agt caa acg gca caa ctt taaattcaat attctactat		579
Met Phe Gln Ser Gln Thr Ala Gln Leu		
170 175		
tgtttatgta ggattggggg agggaaacag ctcataagtc attatgaagg aatttagttc	639	
ctcttcttta ttagtctgta agtaatttc atttgagatt tggatggaca gttgatatta	699	
gctataaaag aaagtcaaac aaaaagagaa aaaaaaaaaaaa aaa	742	

<210> 30
 <211> 176
 <212> PRT
 <213> Homo sapiens

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Tyr Ile Ala Thr Phe Lys Gly Ser Glu Tyr Phe Cys Tyr Asp Leu Ser		
20 25 30		
Gln Asn Pro Ile Gln Ser Ser Asp Glu Ile Thr Leu Ser Phe Lys		
35 40 45		
Thr Leu Gln Arg Asn Gly Leu Met Leu His Thr Gly Lys Ser Ala Asp		
50 55 60		
Tyr Val Asn Leu Ala Leu Lys Asn Gly Ala Val Ser Leu Val Ile Asn		
65 70 75 80		
Leu Gly Ser Gly Ala Phe Glu Ala Leu Val Glu Pro Val Asn Gly Lys		
85 90 95		

Phe Asn Asp Asn Ala Trp His Asp Val Lys Val Thr Arg Asn Leu Arg
 100 105 110
 Gln Val Thr Ile Ser Val Asp Gly Ile Leu Thr Thr Thr Gly Tyr Thr
 115 120 125
 Gln Glu Asp Tyr Thr Met Leu Gly Ser Asp Asp Phe Phe Tyr Val Gly
 130 135 140
 Gly Ser Pro Ser Thr Ala Asp Leu Pro Gly Ser Pro Ile Gln His Glu
 145 150 155 160
 Ser Thr Phe Ala Glu Asp Pro Met Phe Gln Ser Gln Thr Ala Gln Leu
 165 170 175

<210> 31
 <211> 1766
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> 4..1533

<220>
 <221> 3'UTR
 <222> 1534..1766

<220>
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 <222> 1709..1714

<220>
 <221> polyA_site
 <222> 1744..1766

<400> 31

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Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe	
1 5 10 15	
cga gtc tcc gac ctt cag ctc ctg ggt ttc gtg ggc cg ^g agt aag	96
Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys	
20 25 30	
agt gga ctg aag cac gag ctc acc agg gcc ctc cag ctg gtg cag	144
Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln	
35 40 45	
ttt gac tgt acc cct gag ctg ttc aag aag atc aag gag ctg tac gag	192
Phe Asp Cys Thr Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu	
50 55 60	
acc cgc tac gcc aag aag aac tcg gag cct gcc cca cag ccg cac cg ^g	240
Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg	
65 70 75	
ccc ctg gac ccc ctg acc atg cac acc tac gac cg ^g gcc ggc gct	288
Pro Leu Asp Pro Leu Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala	
80 85 90 95	
gtg ccc agg act ccg ctg gca ggc ccc aat att gac tac ccc gtg ctc	336

Val Pro Arg Thr Pro Leu Ala Gly Pro Asn Ile Asp Tyr Pro Val Leu			
100	105	110	
tac gga aag tac tta aac gga ctg gga cgg ttg ccc gcc aag acc ctc			384
Tyr Gly Lys Tyr Leu Asn Gly Leu Gly Arg Leu Pro Ala Lys Thr Leu			
115	120	125	
aag cca gaa gtc cgc ctg gtg aag ctg ccg ttc ttt aat atg ctg gac			432
Lys Pro Glu Val Arg Leu Val Lys Leu Pro Phe Phe Asn Met Leu Asp			
130	135	140	
gag ctg ctg aag ccc acc gaa tta gtc cca cag aac aac gag aag ctt			480
Glu Leu Leu Lys Pro Thr Glu Leu Val Pro Gln Asn Asn Glu Lys Leu			
145	150	155	
cag gag agc ccg tgc atc ttc gca ttg acg cca aga cag gtg gag ttg			528
Gln Glu Ser Pro Cys Ile Phe Ala Leu Thr Pro Arg Gln Val Glu Leu			
160	165	170	175
atc cgg aac tcc agg gaa ctg cag ccc gga gtt aaa gcc gtg cag gtc			576
Ile Arg Asn Ser Arg Glu Leu Gln Pro Gly Val Lys Ala Val Gln Val			
180	185	190	
gtc ctg aga atc tgt tac tca gac acc agc tgc cct cag gag gac cag			624
Val Leu Arg Ile Cys Tyr Ser Asp Thr Ser Cys Pro Gln Glu Asp Gln			
195	200	205	
tac ccg ccc aac atc gct gtg aag gtc aac cac agc tac tgc tcc gtc			672
Tyr Pro Pro Asn Ile Ala Val Lys Val Asn His Ser Tyr Cys Ser Val			
210	215	220	
ccg ggc tac tac ccc tcc aat aag ccc ggg gtg gag ccc aag agg ccc			720
Pro Gly Tyr Tyr Pro Ser Asn Lys Pro Gly Val Glu Pro Lys Arg Pro			
225	230	235	
tgc cgc ccc atc aac ctc acc cac ctc atg tac ctt tcc tcg gcc acc			768
Cys Arg Pro Ile Asn Leu Thr His Leu Met Tyr Leu Ser Ser Ala Thr			
240	245	250	255
aac cgc atc act gtc acc tgg ggg aac tac ggc aag agc tac tcg gtg			816
Asn Arg Ile Thr Val Thr Trp Gly Asn Tyr Gly Lys Ser Tyr Ser Val			
260	265	270	
gcc ctg tac ctg gtg cgg cag ctg acc tca tcg gag ctg ctg cag agg			864
Ala Leu Tyr Leu Val Arg Gln Leu Thr Ser Ser Glu Leu Leu Gln Arg			
275	280	285	
ctg aag acc att ggg gta aag cac ccg gag ctg tgc aag gca ctg gtc			912
Leu Lys Thr Ile Gly Val Lys His Pro Glu Leu Cys Lys Ala Leu Val			
290	295	300	
aag gag aag ctg cgc ctt gat cct gac agc gag atc gcc acc acc ggt			960
Lys Glu Lys Leu Arg Leu Asp Pro Asp Ser Glu Ile Ala Thr Thr Gly			
305	310	315	
gtg cgg gtg tcc atc tgt ccg ctg gtg aag atg cgg ctc tcc gtg			1008
Val Arg Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val			
320	325	330	335
ccc tgc cgg gca gag acc tgc gcc cac ctg cag tgc ttc gac gcc gtc			1056
Pro Cys Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val			
340	345	350	
tcc tac ctg cag atg aac gag aag aag ccc acc tgg atg tgc ccc gtg			1104
Phe Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Met Cys Pro Val			
355	360	365	
tgc gac aag cca gcc ccc tac gac cag ctc atc atc gac ggg ctc ctc			1152
Cys Asp Lys Pro Ala Pro Tyr Asp Gln Leu Ile Ile Asp Gly Leu Leu			
370	375	380	
tcg aag atc ctg agc gag tgt gag gac gcc gac gag atc gag tac ctg			1200
Ser Lys Ile Leu Ser Glu Cys Glu Asp Ala Asp Glu Ile Glu Tyr Leu			
385	390	395	

gtg gac ggc tcg tgg tgc ccg atc cgc gcc gaa aag gag ctc agc tgc	1248
Val Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys	
400 405 410 415	
agc ccg cag ggc gcc atc ctc gtg ctg ggc ccc tcg gac gcc aat ggg	1296
Ser Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly	
420 425 430	
ctc ctg ccc gcc ccc agc gtc aac ggg agc ggt gcc ctg ggc agc acg	1344
Leu Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr	
435 440 445	
ggc ggc ggc ccc gtg ggc agc atg gag aat ggg aag ccg ggc gcc	1392
Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala	
450 455 460	
gat gtg gtg gac ctc acg ctg gac agc tca tcg tcc tcg gag gat gag	1440
Asp Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Glu Asp Glu	
465 470 475	
gag gag gag gaa gag gag gaa gac gag gac gaa gag ggg ccc cgg	1488
Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg	
480 485 490 495	
ccc aag cgc cgc tgc ccc ttc cag aag ggc ctg gtg ccg gcc tgc	1533
Pro Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys	
500 505 510	
tgaccccgcc cgcacacttg actttcctgg tgctcaccac gcagagggggc acggggccagc	1593
ctcgccgcga gagggaggag tgacctttct ttttcctttt attgtcgttc gttttgtttt	1653
tccacccttt tgcctggctc ctggcacctg tacctctgga ctctcctatc gggggattaa	1713
aaaaaaaaagt aaaatgacaa aaaaagatac aaaaagaaa aaaaaaaaaaaa aaa	1766

<210> 32
 <211> 510
 <212> PRT
 <213> Homo sapiens

<400> 32	
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Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe	
35 40 45	
Asp Cys Thr Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr	
50 55 60	
Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro	
65 70 75 80	
Leu Asp Pro Leu Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala Val	
85 90 95	
Pro Arg Thr Pro Leu Ala Gly Pro Asn Ile Asp Tyr Pro Val Leu Tyr	
100 105 110	
Gly Lys Tyr Leu Asn Gly Leu Gly Arg Leu Pro Ala Lys Thr Leu Lys	
115 120 125	
Pro Glu Val Arg Leu Val Lys Leu Pro Phe Phe Asn Met Leu Asp Glu	
130 135 140	
Leu Leu Lys Pro Thr Glu Leu Val Pro Gln Asn Asn Glu Lys Leu Gln	
145 150 155 160	
Glu Ser Pro Cys Ile Phe Ala Leu Thr Pro Arg Gln Val Glu Leu Ile	
165 170 175	
Arg Asn Ser Arg Glu Leu Gln Pro Gly Val Lys Ala Val Gln Val Val	
180 185 190	

Leu Arg Ile Cys Tyr Ser Asp Thr Ser Cys Pro Gln Glu Asp Gln Tyr
 195 200 205
 Pro Pro Asn Ile Ala Val Lys Val Asn His Ser Tyr Cys Ser Val Pro
 210 215 220
 Gly Tyr Tyr Pro Ser Asn Lys Pro Gly Val Glu Pro Lys Arg Pro Cys
 225 230 235 240
 Arg Pro Ile Asn Leu Thr His Leu Met Tyr Leu Ser Ser Ala Thr Asn
 245 250 255
 Arg Ile Thr Val Thr Trp Gly Asn Tyr Gly Lys Ser Tyr Ser Val Ala
 260 265 270
 Leu Tyr Leu Val Arg Gln Leu Thr Ser Ser Glu Leu Leu Gln Arg Leu
 275 280 285
 Lys Thr Ile Gly Val Lys His Pro Glu Leu Cys Lys Ala Leu Val Lys
 290 295 300
 Glu Lys Leu Arg Leu Asp Pro Asp Ser Glu Ile Ala Thr Thr Gly Val
 305 310 315 320
 Arg Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val Pro
 325 330 335
 Cys Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val Phe
 340 345 350
 Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Met Cys Pro Val Cys
 355 360 365
 Asp Lys Pro Ala Pro Tyr Asp Gln Leu Ile Ile Asp Gly Leu Leu Ser
 370 375 380
 Lys Ile Leu Ser Glu Cys Glu Asp Ala Asp Glu Ile Glu Tyr Leu Val
 385 390 395 400
 Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys Ser
 405 410 415
 Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly Leu
 420 425 430
 Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr Gly
 435 440 445
 Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala Asp
 450 455 460
 Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Glu Asp Glu Glu
 465 470 475 480
 Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg Pro
 485 490 495
 Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys
 500 505 510

<210> 33
 <211> 877
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
 <221> CDS
 <222> 11..802

<220>
 <221> 3'UTR

<222> 803..877

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<220>
<221> polyA_signal
<222> 836..841
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<220>
<221> polyA_site
<222> 862..877

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 Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe
 220 225 230 235
 agc acc tgg atc aac cag gtc ata gcc tac aac tgagctcacc acaggccctc 822
 Ser Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn
 240 245
 cccagctcaa cccattaaag acccaggccc tgtcccatca aaaaaaaaaa aaaaa 877

<210> 34
 <211> 264
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..18

<400> 34
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 Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln
 1 5 10
 Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
 15 20 25 30
 Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly Gly Ser Leu
 35 40 45
 Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
 50 55 60
 Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
 65 70 75
 Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser
 80 85 90
 Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu Lys Leu Ala
 95 100 105 110
 Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys Leu Ala Ser
 115 120 125
 Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr Thr Gly Trp
 130 135 140
 Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln
 145 150 155
 Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly
 160 165 170
 Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala Gly Ala Ser
 175 180 185 190
 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
 195 200 205
 Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
 210 215 220
 Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
 225 230 235
 Ile Asn Gln Val Ile Ala Tyr Asn
 240 245

<210> 35
 <211> 1728
 <212> DNA

<213> *Homo sapiens*

<220>
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<220>
<221> CDS
<222> 38..1378

<220>
<221> 3 'UTR
<222> 1379..1728

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<220>
<221> polyA_site
<222> 1713..1728
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	Met Ile Pro Thr Phe Thr	
	-70	
gct ctg ctc tgc ctc ggg ctg agt ctg ggc ccc agg acc cac atg cag	103	
Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Met Gln		
-15 -10 -5		
gca ggg ccc ctc ccc aaa ccc acc ctc tgg gct gag cca ggc tct gtg	151	
Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val		
1 5 10 15		
atc agc tgg ggg aac tct gtg acc atc tgg tgt cag ggg acc ctg gag	199	
Ile Ser Trp Gly Asn Ser Val Thr Ile Trp Cys Gln Gly Thr Leu Glu		
20 25 30		
gct cgg gag tac cgt ctg gat aaa gag gaa agc cca gca ccc tgg gac	247	
Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu Ser Pro Ala Pro Trp Asp		
35 40 45		
aga cag aac cca ctg gag ccc aag aac aag gcc aga ttc tcc atc cca	295	
Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro		
50 55 60		
tcc atg aca gag gac tat gca ggg aga tac cgc tgt tac tat cgc agc	343	
Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr Arg Cys Tyr Tyr Arg Ser		
65 70 75		
cct gta ggc tgg tca cag ccc agt gac ccc ctg gag ctg gtg atg aca	391	
Pro Val Gly Trp Ser Gln Pro Ser Asp Pro Leu Glu Leu Val Met Thr		
80 85 90 95		
gga gcc tac agt aaa ccc acc ctt tca gcc ctg ccg agt cct ctt gtg	439	
Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Leu Val		
100 105 110		
acc tca gaa aag agc gtg acc ctg ctg tgt cag tca cgg agc cca atg	487	
Thr Ser Glu Lys Ser Val Thr Leu Leu Cys Gln Ser Arg Ser Pro Met		
115 120 125		
gac act ttc ctt ctg atc aag gag cgg gca gcc cat ccc cta ctg cat	535	
Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala Ala His Pro Leu Leu His		
130 135 140		
ctg aga tca gag cac gga gct cag cag cac cag gct gaa ttc ccc atg	583	
Leu Arg Ser Glu His Gly Ala Gln Gln His Gln Ala Glu Phe Pro Met		
145 150 155		
agt cct gtg acc tca gtg cac ggg ggg acc tac agg tgc ttc agc tca	631	

Ser Pro Val Thr Ser Val His Gly Gly Thr Tyr Arg Cys Phe Ser Ser			
160	165	170	175
cac ggc ttc tcc cac tac ctg ctg tca cac ccc agt gac ccc ctg gag			679
His Gly Phe Ser His Tyr Leu Leu Ser His Pro Ser Asp Pro Leu Glu			
180	185	190	
ctc ata gtc tca gga tcc ttg gag gat ccc agg ccc tca ccc aca agg			727
Leu Ile Val Ser Gly Ser Leu Glu Asp Pro Arg Pro Ser Pro Thr Arg			
195	200	205	
tcc gtc tca aca gct gca ggc cct gag gac cag ccc ctc atg cct aca			775
Ser Val Ser Thr Ala Ala Gly Pro Glu Asp Gln Pro Leu Met Pro Thr			
210	215	220	
ggg tca gtc ccc cac agt ggt ctg aga agg cac tgg gag gta ctg atc			823
Gly Ser Val Pro His Ser Gly Leu Arg Arg His Trp Glu Val Leu Ile			
225	230	235	
ggg gtc ttg gtg gtc tcc atc ctg ctt ctc tcc ctc ctc ttc ctc			871
Gly Val Leu Val Val Ser Ile Leu Leu Ser Leu Leu Leu Phe Leu			
240	245	250	255
ctc ctc caa cac tgg cgt cag gga aaa cac agg aca ttg gcc cag aga			919
Leu Leu Gln His Trp Arg Gln Gly His Arg Thr Leu Ala Gln Arg			
260	265	270	
cag gct gat ttc caa cgt cct cca ggg gct gcc gag cca gag ccc aag			967
Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala Ala Glu Pro Glu Pro Lys			
275	280	285	
gac ggg ggc cta cag agg agg tcc agc cca gct gac gtc cag gga			1015
Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Gly			
290	295	300	
gaa aac ttc tgt gct gcc gtg aag gac aca cag cct gag gac ggg gtg			1063
Glu Asn Phe Cys Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val			
305	310	315	
gaa atg gac act cgg agc cca cac gat gaa gac ccc cag gca gtg acg			1111
Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr			
320	325	330	335
tat gcc aag gtg aaa cac tcc aga cct agg aga gaa atg gcc tct cct			1159
Tyr Ala Lys Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro			
340	345	350	
ccc tcc cca ctg tct ggg gaa ttc ctg gac aca aag gac aga cag gca			1207
Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala			
355	360	365	
gaa gag gac aga cag atg gac act gag gct gca tct gaa gcc ccc			1255
Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro			
370	375	380	
cag gat gtg acc tac gcc cag ctg cac agc ttt acc ctc aga cag aag			1303
Gln Asp Val Thr Tyr Ala Gln Leu His Ser Phe Thr Leu Arg Gln Lys			
385	390	395	
gca act gag cct cca tcc cag gaa ggg gcc tct cca gct gag ccc			1351
Ala Thr Glu Pro Pro Ser Gln Glu Gly Ala Ser Pro Ala Glu Pro			
400	405	410	415
agt gtc tat gcc act ctg gcc atc cac taatccaggg gggaccacaga			1398
Ser Val Tyr Ala Thr Leu Ala Ile His			
420			
ccccacaagg catggagact caggaccctt gaaggcatgg aagctgcctc cagtagacat			1458
cactgaaccc cagccagccc agacccctga cacagaccac tagaagattc cggaaacgtt			1518
gggagtctacc tgattctgca aagataaata atatccctgc attatcaaaa taaagtagca			1578
gacctctcaa ttccacaatga gttaactgtat aaaacaaaac agaagtcaga caatgtttta			1638
aattgaatga tcatgttaat attacacatc aaaccaatga catggaaaaa tgggagcttc			1698
taatgaggac aaacaaaaaaa aaaaaaaaaa			1728

<210> 36
 <211> 447
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..23

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 Pro Arg Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
 -5 1 5
 Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp
 10 15 20 25
 Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu
 30 35 40
 Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
 45 50 55
 Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
 60 65 70
 Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro
 75 80 85
 Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala
 90 95 100 105
 Leu Pro Ser Pro Leu Val Thr Ser Glu Lys Ser Val Thr Leu Leu Cys
 110 115 120
 Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala
 125 130 135
 Ala His Pro Leu Leu His Leu Arg Ser Glu His Gly Ala Gln Gln His
 140 145 150
 Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr
 155 160 165
 Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His
 170 175 180 185
 Pro Ser Asp Pro Leu Glu Leu Ile Val Ser Gly Ser Leu Glu Asp Pro
 190 195 200
 Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp
 205 210 215
 Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg
 220 225 230
 His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu
 235 240 245
 Ser Leu Leu Leu Phe Leu Leu Gln His Trp Arg Gln Gly Lys His
 250 255 260 265
 Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala
 270 275 280
 Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro
 285 290 295
 Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asp Thr
 300 305 310
 Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp Glu
 315 320 325
 Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro Arg

330	335	340	345
Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp			
350	355	360	
Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala			
365	370	375	
Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser			
380	385	390	
Phe Thr Leu Arg Gln Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly			
395	400	405	
Ala Ser Pro Ala Glu Pro Ser Val Tyr Ala Thr Leu Ala Ile His			
410	415	420	
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<222> 1742..1757			
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cggcccccgg cttgcgtcgg cgaagaggag agcaaggctg ttctgggatc cggccgtcg	180		
gcggcaagag gcttgtctgt ccgggttgcc ggaaccagga gaacccagag ggaaaccgag	240		
gcaaaggagc ggcgctttt actagagaga gcgcgagcgg aagaggcgg agcaggagcg	300		
cgcgagggag catcgagcgc agcggagac atg agg acc tac tgg ctg cac agc	353		
Met Arg Thr Tyr Trp Leu His Ser			
-20			
gtc tgg gtg ctg ggc ttt ttc ctg tcc ttc tca ttg caa gga ctg	401		
Val Trp Val Leu Gly Phe Phe Leu Ser Leu Phe Ser Leu Gln Gly Leu			
-15	-10	-5	1
cct gtt cgc agc gtg gat ttt aac cga ggc acg gac aac atc acc gtg	449		
Pro Val Arg Ser Val Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val			
5	10	15	
agg cag ggg gac aca gcc atc ctc agg tgc gtt gta gaa gac aag aac	497		
Arg Gln Gly Asp Thr Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn			
20	25	30	
tca aag gtg gcc tgg ttg aac cgt tct ggc atc att ttt gct gga cat	545		

Ser Lys Val Ala Trp Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His			
35	40	45	
gac aag tgg tct ctg gac cca cgg gtt gag ctg gag aaa cgc cat tct			593
Asp Lys Trp Ser Leu Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser			
50	55	60	65
ctg gaa tac agc ctc cga atc cag aag gtg gat gtc tat gat gag ggt			641
Leu Glu Tyr Ser Leu Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly			
70	75	80	
tcc tac act tgc tca gtt cag aca cag cat gag ccc aag acc tcc caa			689
Ser Tyr Thr Cys Ser Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln			
85	90	95	
gtt tac ttg atc gta caa gtc cca cca aag atc tcc aat atc tcc tcg			737
Val Tyr Leu Val Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser			
100	105	110	
gat gtc act gtg aat gag ggc agc aac gtg act ctg gtc tgc atg gcc			785
Asp Val Thr Val Asn Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala			
115	120	125	
aat ggc cgt cct gaa cct gtt atc acc tgg aga cac ctt aca cca act			833
Asn Gly Arg Pro Glu Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr			
130	135	140	145
gga agg gaa ttt gaa gga gaa gaa tat ctg gag atc ctt ggc atc			881
Gly Arg Glu Phe Glu Gly Glu Glu Tyr Leu Glu Ile Leu Gly Ile			
150	155	160	
acc agg gag cag tca ggc aaa tat gag tgc aaa gct gcc aac gag gtc			929
Thr Arg Glu Gln Ser Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val			
165	170	175	
tcc tcg gcg gat gtc aaa caa gtc aag gtc act gtg aac tat cct ccc			977
Ser Ser Ala Asp Val Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro			
180	185	190	
act atc aca gaa tcc aag agc aat gaa gcc acc aca gga cga caa gct			1025
Thr Ile Thr Glu Ser Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala			
195	200	205	
tca ctc aaa tgt gag gcc tcg gca gtg cct gca cct gac ttt gag tgg			1073
Ser Leu Lys Cys Glu Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp			
210	215	220	225
tac cgg gat gac act agg ata aat agt gcc aat ggc ctt gag att aag			1121
Tyr Arg Asp Asp Thr Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys			
230	235	240	
agc acg gag ggc cag tct tcc ctg acg gtg acc aac gtc act gag gag			1169
Ser Thr Glu Gly Gln Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu			
245	250	255	
cac tac ggc aac tac acc tgt gtg gct gcc aac aag ctg ggg gtc acc			1217
His Tyr Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr			
260	265	270	
aat gcc agc cta gtc ctt ttc aaa cgt gtt tta ccc aca atc ccc cac			1265
Asn Ala Ser Leu Val Leu Phe Lys Arg Val Leu Pro Thr Ile Pro His			
275	280	285	
ccc att caa gaa att ggt acc acc gtg cac ttc aag caa aaa ggc atc			1313
Pro Ile Gln Glu Ile Gly Thr Thr Val His Phe Lys Gln Lys Gly Ile			
290	295	300	305
ttc ctc tct gag tct cag agg ggt gag aca acc aag atc act ctc aac			1361
Phe Leu Ser Glu Ser Gln Arg Gly Glu Thr Thr Lys Ile Thr Leu Asn			
310	315	320	
tgt gga aat cta ttc ttg cgg aac tta cat ccc acc agt gat caa gag			1409
Cys Gly Asn Leu Phe Leu Arg Asn Leu His Pro Thr Ser Asp Gln Glu			
325	330	335	

Thr Val Thr Asn Val Thr Glu Glu His Tyr Gly Asn Tyr Thr Cys Val
 250 255 260 265
 Ala Ala Asn Lys Leu Gly Val Thr Asn Ala Ser Leu Val Leu Phe Lys
 270 275 280
 Arg Val Leu Pro Thr Ile Pro His Pro Ile Gln Glu Ile Gly Thr Thr
 285 290 295
 Val His Phe Lys Gln Lys Gly Ile Phe Leu Ser Glu Ser Gln Arg Gly
 300 305 310
 Glu Thr Thr Lys Ile Thr Leu Asn Cys Gly Asn Leu Phe Leu Arg Asn
 315 320 325
 Leu His Pro Thr Ser Asp Gln Glu Pro Gln Arg Leu Trp Thr Leu Cys
 330 335 340 345
 Cys Leu Leu Pro Arg Lys Gly Gln His Arg Ile Tyr Gly Gln Cys
 350 355 360

<210> 39
 <211> 2818
 <212> DNA
 <213> Homo sapiens

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<220>
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 <222> 81..1517

<220>
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<220>
 <221> polyA_site
 <222> 2804..2818

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 ctgcggagtc agacggcgct atg tac gcc ctc ttc ctc ctg gcc agc ctc ctg 113
 Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu
 1 5 10
 ggc gcg gct cta gcc ggc ccg gtc ctt gga ctg aaa gaa tgc acc agg 161
 Gly Ala Ala Leu Ala Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg
 15 20 25
 ggc tcg gca gtg tgg tgc cag aat gtg aag acg gcg tcc gac tgc ggg 209
 Gly Ser Ala Val Trp Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly
 30 35 40
 gca gtg aag cac tgc ctg cag acc gtt tgg aac aag cca aca gtg aaa 257
 Ala Val Lys His Cys Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys
 45 50 55
 tcc ctt ccc tgc gac ata tgc aaa gac gtt gtc acc gca gct ggt gat 305
 Ser Leu Pro Cys Asp Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp

60	65	70	75													
atg	ctg	aag	gac	aat	gcc	act	gag	gag	gag	atc	ctt	gtt	tac	ttg	gag	353
Met	Leu	Lys	Asp	Asn	Ala	Thr	Glu	Glu	Glu	Ile	Leu	Val	Tyr	Leu	Glu	
80	85	90														
aag	acc	tgt	gac	tgg	ctt	ccg	aaa	ccg	aac	atg	tct	gct	tca	tgc	aag	401
Lys	Thr	Cys	Asp	Trp	Leu	Pro	Lys	Pro	Asn	Met	Ser	Ala	Ser	Cys	Lys	
95	100	105														
gag	ata	gtg	gac	tcc	tac	ctc	cct	gtc	atc	ctg	gac	atc	att	aaa	gga	449
Glu	Ile	Val	Asp	Ser	Tyr	Leu	Pro	Val	Ile	Leu	Asp	Ile	Ile	Lys	Gly	
110	115	120														
gaa	atg	agc	cgt	cct	ggg	gag	gtg	tgc	tct	gct	ctc	aac	ctc	tgc	gag	497
Glu	Met	Ser	Arg	Pro	Gly	Glu	Val	Cys	Ser	Ala	Leu	Asn	Leu	Cys	Glu	
125	130	135														
tct	ctc	cag	cac	cta	gca	gag	ctg	aat	cac	cag	aag	cag	ctg	gag		545
Ser	Leu	Gln	His	Leu	Ala	Glu	Leu	Asn	His	Gln	Lys	Gln	Leu	Glu		
140	145	150													155	
tcc	aat	aag	atc	cca	gag	ctg	gac	atg	act	gag	gtg	gtg	gcc	ccc	ttc	593
Ser	Asn	Lys	Ile	Pro	Glu	Leu	Asp	Met	Thr	Glu	Val	Val	Ala	Pro	Phe	
160	165	170														
atg	gcc	aac	atc	cct	ctc	ctc	tac	cct	cag	gac	ggc	ccc	cgc	agc		641
Met	Ala	Asn	Ile	Pro	Leu	Leu	Leu	Tyr	Pro	Gln	Asp	Gly	Pro	Arg	Ser	
175	180	185														
aag	ccc	cag	cca	aag	gat	aat	ggg	gac	gtt	tgc	cag	gac	tgc	att	cag	689
Lys	Pro	Gln	Pro	Lys	Asp	Asn	Gly	Asp	Val	Cys	Gln	Asp	Cys	Ile	Gln	
190	195	200														
atg	gtg	act	gac	atc	cag	act	gct	gta	cg	acc	tcc	acc	ttt	gtc		737
Met	Val	Thr	Asp	Ile	Gln	Thr	Ala	Val	Arg	Thr	Asn	Ser	Thr	Phe	Val	
205	210	215														
cag	gcc	ttg	gtg	gaa	cat	gtc	aag	gag	gag	tgt	gac	cgc	ctg	ggc	cct	785
Gln	Ala	Leu	Val	Glu	His	Val	Lys	Glu	Glu	Cys	Asp	Arg	Leu	Gly	Pro	
220	225	230													235	
ggc	atg	gcc	gac	ata	tgc	aag	aac	tat	atc	agc	cag	tat	tct	gaa	att	833
Gly	Met	Ala	Asp	Ile	Cys	Lys	Asn	Tyr	Ile	Ser	Gln	Tyr	Ser	Glu	Ile	
240	245	250														
gct	atc	cag	atg	atg	cac	atg	cag	gat	cag	caa	ccc	aag	gag	atc		881
Ala	Ile	Gln	Met	Met	His	Met	Gln	Asp	Gln	Gln	Pro	Lys	Glu	Ile		
255	260	265														
tgt	gcg	ctg	gtt	ggg	ttc	tgt	gat	gag	gtg	aaa	gag	atg	ccc	atg	cag	929
Cys	Ala	Leu	Val	Gly	Phe	Cys	Asp	Glu	Val	Lys	Glu	Met	Pro	Met	Gln	
270	275	280														
act	ctg	gtc	ccc	gcc	aaa	gtg	gcc	tcc	aag	aat	gtc	atc	cct	gcc	ctg	977
Thr	Leu	Val	Pro	Ala	Lys	Val	Ala	Ser	Lys	Asn	Val	Ile	Pro	Ala	Leu	
285	290	295														
gaa	ctg	gtg	gag	ccc	att	aag	aag	cac	gag	gtc	cca	gca	aag	tct	gat	1025
Glu	Leu	Val	Glu	Pro	Ile	Lys	Lys	His	Glu	Val	Pro	Ala	Lys	Ser	Asp	
300	305	310													315	
gtt	tac	tgt	gag	gtg	tgt	gaa	ttc	ctg	gtg	aag	gag	gtg	acc	aag	ctg	1073
Val	Tyr	Cys	Glu	Val	Cys	Glu	Phe	Leu	Val	Lys	Glu	Val	Thr	Lys	Leu	
320	325	330														
att	gac	aac	aag	act	gag	aaa	gaa	ata	ctc	gac	gct	ttt	gac	aaa		1121
Ile	Asp	Asn	Lys	Thr	Glu	Lys	Ile	Leu	Asp	Ala	Phe	Asp	Lys			
335	340	345														
atg	tgc	tcg	aag	ctg	ccg	aag	tcc	ctg	tcg	gaa	gag	tgc	cag	gag	gtg	1169
Met	Cys	Ser	Lys	Leu	Pro	Lys	Ser	Leu	Ser	Glu	Glu	Cys	Gln	Glu	Val	
350	355	360														
gtg	gac	acg	tac	ggc	agc	tcc	atc	ctg	tcc	atc	ctg	ctg	gag	gag	gtc	1217

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<212> PRT
<213> *Homo sapiens*

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20          25          30
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys

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35	40	45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser	Leu Pro Cys Asp	
50	55	60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met	Leu Lys Asp Asn	
65	70	75
Ala Thr Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr	Cys Asp Trp	
85	90	95
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu	Ile Val Asp Ser	
100	105	110
Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu	Met Ser Arg Pro	
115	120	125
Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser	Leu Gln Lys His	
130	135	140
Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser	Asn Lys Ile Pro	
145	150	155
Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met	Ala Asn Ile Pro	
165	170	175
Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys	Pro Gln Pro Lys	
180	185	190
Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met	Val Thr Asp Ile	
195	200	205
Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln	Ala Leu Val Glu	
210	215	220
His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly	Met Ala Asp Ile	
225	230	235
Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala	Ile Gln Met Met	
245	250	255
Met His Met Gln Asp Gln Gln Pro Lys Glu Ile Cys	Ala Leu Val Gly	
260	265	270
Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln Thr	Leu Val Pro Ala	
275	280	285
Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu Glu	Leu Val Glu Pro	
290	295	300
Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp Val	Tyr Cys Glu Val	
305	310	315
Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile	Asp Asn Asn Lys	
325	330	335
Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys Met	Cys Ser Lys Leu	
340	345	350
Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val Val	Asp Thr Tyr Gly	
355	360	365
Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val Ser	Pro Glu Leu Val	
370	375	380
Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg Leu	Pro Ala Leu Thr	
385	390	395
Val His Val Thr Gln Pro Lys Asp Gly Gly Phe Cys	Glu Val Cys Lys	
405	410	415
Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu Lys	Asn Ser Thr Lys	
420	425	430
Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys Ser	Phe Leu Pro Asp	
435	440	445
Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala Glu	Tyr Glu Pro Val	
450	455	460
Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu Pro	Ser Cys Ala	
465	470	475

<210> 41
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 <212> DNA
 <213> Homo sapiens

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<220>
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 <222> 547..770

<220>
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 <222> 739..744

<220>
 <221> polyA_site
 <222> 755..770

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 caagagtctg atcagcagcc tcttcctcct ccaggaccca gaagccctga gcttatcccc 120
 atg gag ctc tgc cgg tcc ctg gcc ctg ctg ggg ggc tcc ctg ggc ctg 168
 Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu
 -35 -30 -25
 atg ttc tgc ctg att gct ttg agc acc gat ttc tgg ttt gag gct gtg 216
 Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val
 -20 -15 -10
 ggt ccc acc cac tca gct cac tcg ggc ctc tgg cca aca ggg cat ggg 264
 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly
 -5 1 5 10
 gac atc ata tca ggc cac ggc ccg ctt gtc tca acc acc gca gcc ttt 312
 Asp Ile Ile Ser Gly His Pro Leu Val Ser Thr Thr Ala Ala Phe
 15 20 25
 gct gca ggt aag gac tct gga ctg gac tgg ggc atc gcg agc cag cga 360
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg
 30 35 40
 att cct gcc gag gag ctg agc cat ctc tct tgt cct tgt ccc cag cca 408
 Ile Pro Ala Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro
 45 50 55
 tct cca tgg tgg tgg cca tgg cgg tgt aca cca gcg agc ggt ggg acc 456
 Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
 60 65 70 75
 agc ctc cac acc ccc aga tcc aga cct tct tct cct ggt cct tct acc 504
 Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr
 80 85 90
 tgg gct ggg tct cag cta tcc tct tgc tct gta cag gtg ccc 546
 Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
 95 100 105
 tgagcctggg tgctcaactgt ggccgtccccc gtcctggcta tggaaaccttg tgagcagaag 606

gcaagagcgg caagatgagt tttgagcggt gtattccaaa ggcctcatct ggagcctcg 666
 gaaagtctgg tcccacatct gccgcgcctt ccagcccttc cccagccctt cctcttgttt 726
 cttcattcat tcaacaaaat ttggctggaa aaaaaaaaaa aaaa 770

<210> 42
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..37

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 Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val
 -20 -15 -10
 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly
 -5 1 5 10
 Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe
 15 20 25
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg
 30 35 40
 Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro
 45 50 55
 Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
 60 65 70 75
 Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr
 80 85 90
 Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
 95 100 105

<210> 43
 <211> 1340
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..135

<220>
 <221> CDS
 <222> 136..501

<220>
 <221> 3'UTR
 <222> 502..1340

<220>
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 <222> 1232..1237

<220>
 <221> polyA_site

<222> 1255..1340

<400> 43

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ccccactagg tgaag atg tca gcc cag gag agc tgc ctc agc ctc atc aag	171
Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys	
1 5 10	
tac ttc ctc ttc gtt ttc aac ctc ttc ttc gtc ctc ggc agc ctg	219
Tyr Phe Leu Phe Val Phe Asn Leu Phe Phe Val Leu Gly Ser Leu	
15 20 25	
atc ttc tgc ttc ggc atc tgg atc ctc att gac aag acc agc ttc gtg	267
Ile Phe Cys Phe Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val	
30 35 40	
tcc ttt gtg ggc ttg gcc ttc gtg cct ctg cag atc tgg tcc aaa gtc	315
Ser Phe Val Gly Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val	
45 50 55 60	
ctg gcc atc tca gga atc ttc acc atg ggc atc gcc ctc ctg ggt tgt	363
Leu Ala Ile Ser Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys	
65 70 75	
gtg ggg gcc ctc aag gag ctc cgc tgc ctc ctg ggc ctg tat ttt ggg	411
Val Gly Ala Leu Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly	
80 85 90	
atg ctg ctg ctc ctg ttt gcc aca cag atc acc ctg gga atc ctc atc	459
Met Leu Leu Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile	
95 100 105	
tcc act cag cgg gcc agc tgg agc gaa gct tgc ggg acg tcg	501
Ser Thr Gln Arg Ala Ser Trp Ser Glu Ala Cys Gly Thr Ser	
110 115 120	
tagagaaaac catccaaaag tacggcacca accccgagga gaccgcggcc gaggagagct	561
gggactatgt gcagttccag ctgcgcgtct gcggctggca ctacccgcag gactgggtcc	621
aagtccatcat cctgagaggt aacgggtcgg aggcgcaccc cgtagccctgc tcctgctaca	681
acttgtcggc gaccaacgac tccacaatcc tagataaggt gatcttgcac cagctcagca	741
ggcttggaca cctggcgccg tccagacaca gtgcagacat ctgcgcgtgc cctgcagaga	801
gccacatcta cccgcaggcc tgcgcgcagg gcctccagaa gtggctgcac aacaacctta	861
tttccatagt gggcatttgc ctggggcgtcg gcctactcga gctcgggttc atgacgctct	921
cgtatattcct gtgcagaaac ctggaccacg tctacaaccg gctcgctcga taccgttagg	981
ccccgcctc cccaaagtcc cgcggccccc ccgtcaacgt cgctgggcac ttccctgtcg	1041
cctgtaaata ttgtttaat ccccagttcg cctggagccc tcctccttca cattcccttg	1101
gggacccacg tggctgcgtg ccctgtcgtc tgcacccct cccacgggac ctggggcttt	1161
cgtccacacg ttcctgtccc catctgtcgg cctaccacca cccacaaagat tattttcac	1221
ccaaacctca aataaattccc ctgcgtttt ggtaaaaaaaaaaaaaaaaaaaaaaaaa	1281
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa amaaaaaaaaa aaaaaaaaaa	1340

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<211> 122

<212> PRT

<213> Homo sapiens

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Val Phe Asn Leu Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe

20 25 30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly

35 40 45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
 50 55 60
 Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
 65 70 75 80
 Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
 85 90 95
 Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
 100 105 110
 Ala Ser Trp Ser Glu Ala Cys Gly Thr Ser
 115 120

<210> 45

<211> 1999

<212> DNA

<213> Homo sapiens

<220>

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<221> CDS

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<221> polyA_site

<222> 1956..1999

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tccgcagtcc cagccgagcc gcgcacccttc cggccgtccc caccccacct cgccgcc 117

atg cgc ctc cgc cgc cta gcg ctg ttc ccg ggt gtg gcg ctg ctt ctt 165

Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu

-20 -15 -10

gcc gcg gcc cgc ctc gct gcc tcc gac gtg cta gaa ctc acg gac 213

Ala Ala Ala Arg Leu Ala Ala Ser Asp Val Leu Glu Leu Thr Asp

-5 1 5

gac aac ttc gag agt cgc atc tcc gac acg ggc tct gcg ggc ctc atg 261

Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met

10 15 20

ctc gtc gag ttc gct ccc tgg tgt gga cac tgc aag aga ctt gca 309

Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala

25 30 35 40

cct gag tat gaa gct gca gct acc aga tta aaa gga ata gtc cca tta 357

Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu

45 50 55

gca aag gtt gat tgc act gcc aac act aac acc tgt aat aaa tat gga 405

Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly

60	65	70	
gtc agt gga tat cca acc ctg aag ata ttt aga gat ggt gaa gaa gca			453
Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala			
75	80	85	
ggt gct tat gat gga cct agg act gct gat gga att gtc agc cac ttg			501
Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu			
90	95	100	
aag aag cag gca gga cca gct tca gtg cct ctc agg act gag gaa gaa			549
Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu			
105	110	115	120
ttt aag aaa ttc att agt gat aaa gat gcc tct ata gta ggt ttt ttc			597
Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe			
125	130	135	
gat gat tca ttc agt gag gct cac tcc gag ttc cta aaa gca gcc agc			645
Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser			
140	145	150	
aac ttg agg gat aac tac cga ttt gca cat acg aat gtt gag tct ctg			693
Asn Leu Arg Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu			
155	160	165	
gtg aac gag tat gat gat aat gga gag ggt atc atc tta ttt cgt cct			741
Val Asn Glu Tyr Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro			
170	175	180	
tca cat ctc act aac aag ttt gag gac aag act gtg gca tat aca gag			789
Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu			
185	190	195	200
caa aaa atg acc agt ggc aaa att aaa aag ttt atc cag gaa aac att			837
Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile			
205	210	215	
ttt ggt atc tgc cct cac atg aca gaa gac aat aaa gat ttg ata cag			885
Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln			
220	225	230	
ggc aag gac tta ctt att gct tac tat gat gtg gac tat gaa aag aac			933
Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn			
235	240	245	
gct aaa ggt tcc aac tac agg aga aac agg gta atg atg gtg gca aag			981
Ala Lys Gly Ser Asn Tyr Arg Arg Asn Arg Val Met Met Val Ala Lys			
250	255	260	
aaa ttc ctg gat gct ggg cac aaa ctc aac ttt gct gta gct agc cgc			1029
Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg			
265	270	275	280
aaa acc ttt agc cat gaa ctt tct gat ttt ggc ttg gag agc act gct			1077
Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala			
285	290	295	
gga gag att cct gtt gtt gct atc aga act gct aaa gga gag aag ttt			1125
Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe			
300	305	310	
gtc atg cag gag gag ttc tcg cgt gat ggg aag gct ctg gag agg ttc			1173
Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe			
315	320	325	
ctg cag gat tac ttt gat ggc aat ctg aag aga tac ctg aag tct gaa			1221
Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu			
330	335	340	
cct atc cca gag agc aat gat ggg cct gtg aag gta gtg gta gca gag			1269
Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Ala Glu			
345	350	355	360
aat ttt gat gaa ata gtg aat aat gaa aat aaa gat gtg ctg att gaa			1317

Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu			
365	370	375	
ttt tat gcc cct tgg tgt ggt cat tgt aag aac ctg gag ccc aag tat			1365
Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr			
380	385	390	
aaa gaa ctt ggc gag aag ctc agc aaa gac cca aat atc gtc ata gcc			1413
Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala			
395	400	405	
aag atg gat gcc aca gcc aat gat gtg cct tct cca tat gaa gtc aga			1461
Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg			
410	415	420	
ggt ttt cct acc ata tac ttc tct cca gcc aac aag aag cta aat cca			1509
Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro			
425	430	435	440
aag aaa tat gaa ggt ggc cgt gaa tta agt gat ttt att agc tat cta			1557
Lys Lys Tyr Glu Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu			
445	450	455	
caa aga gaa gct aca atc ccc cct gta att caa gaa gaa aaa ccc aag			1605
Gln Arg Glu Ala Thr Ile Pro Pro Val Ile Gln Glu Glu Lys Pro Lys			
460	465	470	
aag aag aag gca cag gag gat ctc taaaggagta gccaaacacc			1652
Lys Lys Lys Ala Gln Glu Asp Leu			
475	480		
actttgtaaa aggactcttc catcagagat gggaaaacca ttggggagga ctaggaccca			1712
tatgggaatt attacctctc agggccgaga ggacagaatg gatataatct gaatcctgtt			1772
aaattttctc taaactgttt ctagctgca ctgttatgg aaataccagg accagtttat			1832
gtttgtggtt ttggggaaaa ttatgtgt tgggggaaat gttgtgggg tggggtttag			1892
ttgggggtat ttctaattt ttttgtaca ttggAACAG tgacaataaa tgagacccct			1952
tttaaaaaaaa aaaaaaaaaa aaaaaawaaaaa aaaaaaaaaa			1999

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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

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 -5 1 5
 Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
 10 15 20
 Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
 25 30 35 40
 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
 45 50 55
 Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly
 60 65 70
 Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala
 75 80 85
 Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu
 90 95 100

Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu
 105 110 115 120
 Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe
 125 130 135
 Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser
 140 145 150
 Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu
 155 160 165
 Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro
 170 175 180
 Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu
 185 190 195 200
 Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile
 205 210 215
 Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln
 220 225 230
 Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn
 235 240 245
 Ala Lys Gly Ser Asn Tyr Arg Arg Asn Arg Val Met Met Val Ala Lys
 250 255 260
 Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg
 265 270 275 280
 Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala
 285 290 295
 Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe
 300 305 310
 Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe
 315 320 325
 Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu
 330 335 340
 Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Val Ala Glu
 345 350 355 360
 Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
 365 370 375
 Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
 380 385 390
 Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
 395 400 405
 Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
 410 415 420
 Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
 425 430 435 440
 Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
 445 450 455
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 460 465 470
 Lys Lys Lys Ala Gln Glu Asp Leu
 475 480

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 <211> 836
 <212> DNA
 <213> Homo sapiens

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<222> 1..153

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<222> 722..836

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 gatgctgtgg ttggatattt agaggacatt atc atg gat gac gag ttc cag tta 174
 Met Asp Asp Glu Phe Gln Leu
 1 5
 tta cag aga aat ttc atg gac aag tac tac ctg gag ttt gaa gac aca 222
 Leu Gln Arg Asn Phe Met Asp Lys Tyr Tyr Leu Glu Phe Glu Asp Thr
 10 15 20
 gaa gag aat aaa ctc atc tac aca cct att ttt aat gaa tac att tct 270
 Glu Glu Asn Lys Leu Ile Tyr Thr Pro Ile Phe Asn Glu Tyr Ile Ser
 25 30 35
 ttg gta gaa aaa tac att gaa gaa cag ctg ctg cag cgg att cct gag 318
 Leu Val Glu Lys Tyr Ile Glu Glu Gln Leu Leu Gln Arg Ile Pro Glu
 40 45 50 55
 ttc aac atg gca gcc ttc acc aca aca tta cag cac cat aag gat gaa 366
 Phe Asn Met Ala Ala Phe Thr Thr Leu Gln His His Lys Asp Glu
 60 65 70
 gtg gct ggt gac ata ttc gac atg ctg ctc acc ttc aca gat ttt ctg 414
 Val Ala Gly Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu
 75 80 85
 gct ttt aaa gaa atg ttt ttg gac tac aga gca gaa aaa gaa ggc cga 462
 Ala Phe Lys Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg
 90 95 100
 gga ctg gac tta agc agt ggc tta gtg gtg act tca ttg tgc aaa tca 510
 Gly Leu Asp Leu Ser Ser Gly Leu Val Val Thr Ser Leu Cys Lys Ser
 105 110 115
 tct tct ctg cca gct tcc cag aac aat ctg cgg cac taggtcctac 556
 Ser Ser Leu Pro Ala Ser Gln Asn Asn Leu Arg His
 120 125 130
 ctccagccaa tgaatggat cattctggat gtcaccagcc caataggctc agctcatgtat 616
 gacagaacac atcttggaaa gactgactct gttatgttaac tcttcattta tgttaagtat 676
 taataggtca aaacccaaat gacctaaccct tcctggacct atttcaaaaaaaa aaaaaaaaaa 736
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 796
 aaaaaaaaaa aaaaaaaaaa aaaqaaaaaa aaaaaaaaaat 836

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<211> 131
<212> PRT
<213> *Homo sapiens*

<400> 48

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 Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln
 35 40 45
 Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr
 50 55 60
 Leu Gln His His Lys Asp Glu Val Ala Gly Asp Ile Phe Asp Met Leu
 65 70 75 80
 Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys Glu Met Phe Leu Asp Tyr
 85 90 95
 Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp Leu Ser Ser Gly Leu Val
 100 105 110
 Val Thr Ser Leu Cys Lys Ser Ser Ser Leu Pro Ala Ser Gln Asn Asn
 115 120 125
 Leu Arg His
 130

<210> 49
 <211> 862
 <212> DNA
 <213> Homo sapiens

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 <222> 1..195

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<220>
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 <222> 847..862

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 cggaggcagc tggggaggc tcgagcgatgt gaccaggccg ccatcgctcg tctcttcctc 120
 tctcctgcgg cctcctgtct cgtaaataac tttttactc taaaagaaaga aagacaaaag 180
 tagtcgtccg ccccc atg cat ccc ttc tac acc cgg gcc gcc acc atg ata 231
 Met His Pro Phe Tyr Thr Arg Ala Ala Thr Met Ile
 1 5 10
 ggc gag atc gcc gcc gtg tcc ttc atc tcc aag ttt ctc cgc acc 279
 Gly Glu Ile Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr
 15 20 25
 aag ggg ctc acg agc gag cga cag ctg cag acc ttc agc cag agc ctg 327
 Lys Gly Leu Thr Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu
 30 35 40
 cag gag ctg ctg gca gaa cat tat aaa cat cac tgg ttc cca gaa aag 375
 Gln Glu Leu Leu Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys
 45 50 55 60

cca tgc aag gga tcg ggt tac cgt tgt att cgc atc aac cat aaa atg	423
Pro Cys Lys Gly Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met	
65 70 75	
gat cct ctg att gga cag gca gca cag cgg att gga ctg agc agt cag	471
Asp Pro Leu Ile Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln	
80 85 90	
gag ctg ttc agg ctt ctc cca agt gaa ctc aca ctc tgg gtt gac ccc	519
Glu Leu Phe Arg Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro	
95 100 105	
tat gaa gtg tcc tac aga att gga gag gat ggc tcc atc tgt gtg ctg	567
Tyr Glu Val Ser Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu	
110 115 120	
tat gaa gcc tca cca gca gga ggt agc act caa aac agc acc aac gtg	615
Tyr Glu Ala Ser Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val	
125 130 135 140	
caa atg gta gac agc cga atc agc tgt aag gag gaa ctt ctc ttg ggc	663
Gln Met Val Asp Ser Arg Ile Ser Cys Lys Glu Leu Leu Gly	
145 150 155	
aga acg agc cct tcc aaa aac tac aat atg atg act gta tca agt	708
Arg Thr Ser Pro Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser	
160 165 170	
taagatatacg tctgtggatg gatcatctga tgatgatgga taaaatttgat ttttgctttg	768
ggggcgtcc tcttggggat ggattatgga atttaaacca tgtcacagct gtgaagatct	828
ggcacaagat agaatggcaa aaaaaaaaaaaa aaaa	862

<210> 50
<211> 171
<212> PRT
<213> Homo sapiens

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20 25 30	
Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu Gln Glu Leu Leu	
35 40 45	
Ala Glu His Tyr Lys His Trp Phe Pro Glu Lys Pro Cys Lys Gly	
50 55 60	
Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Leu Ile	
65 70 75 80	
Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln Glu Leu Phe Arg	
85 90 95	
Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Ser	
100 105 110	
Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Ala Ser	
115 120 125	
Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val Gln Met Val Asp	
130 135 140	
Ser Arg Ile Ser Cys Lys Glu Leu Leu Leu Gly Arg Thr Ser Pro	
145 150 155 160	
Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser	
165 170	

<210> 51
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<212> DNA
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<220>
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 <222> 62..778

<220>
 <221> 3'UTR
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<220>
 <221> polyA_signal
 <222> 912..917

<220>
 <221> polyA_site
 <222> 932..947

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 a atg cca ctc ccc ctc cca tca gcg ttc gtg ctg tca gcc ttg cag cct 109
 Met Pro Leu Pro Leu Pro Ser Ala Phe Val Leu Ser Ala Leu Gln Pro
 -20 -15 -10
 tct cct act cat tcc agc tcc aat acc cag cgg ctg cca gac cga gtg 157
 Ser Pro Thr His Ser Ser Asn Thr Gln Arg Leu Pro Asp Arg Val
 -5 1 5 10
 acc ggc ggc ttc tca gtg aat gga cag ctc att ggc aac aag gcc agg 205
 Thr Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg
 15 20 25
 agc cct ggg cag cat gac ggc acg tac ttc ggg cgg ctg gga atc gca 253
 Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala
 30 35 40
 aac cct gcc acg gac ttt cag ttg gaa gtg act cct cag aac att acg 301
 Asn Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr
 45 50 55
 ctg aac ccc ggc ttt ggt ggg cct gtg ttt tcc tgg agg gac caa gct 349
 Leu Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala
 60 65 70 75
 gtg ctg cgg cag gac ggg gtg gtg acc atc aac aag aag agg aac 397
 Val Leu Arg Gln Asp Gly Val Val Val Thr Ile Asn Lys Lys Arg Asn
 80 85 90
 ctg gtg gtg tct gtg gac gac ggt ggc acc ttt gag gtt gtt ttg cac 445
 Leu Val Val Ser Val Asp Asp Gly Gly Thr Phe Glu Val Val Leu His
 95 100 105
 cga gtg tgg aag ggg agc tcg gtc cac cag gac ttc ctg ggc ttc tat 493
 Arg Val Trp Lys Gly Ser Ser Val His Gln Asp Phe Leu Gly Phe Tyr
 110 115 120
 gtg ctg gac agt cat cgg atg tca gcc cgg acg cac ggg ctg ctg ggg 541
 Val Leu Asp Ser His Arg Met Ser Ala Arg Thr His Gly Leu Leu Gly
 125 130 135
 caa ttt ttc cac ccc atc ggt ttt gaa gtg tct gac atc cac cca ggc 589

Gln	Phe	Phe	His	Pro	Ile	Gly	Phe	Glu	Val	Ser	Asp	Ile	His	Pro	Gly	
140							145			150				155		
tct	gac	ccc	aca	aag	cca	gat	gcc	acg	atg	gtg	gtg	agg	aac	cgc	cg	637
Ser	Asp	Pro	Thr	Lys	Pro	Asp	Ala	Thr	Met	Val	Val	Arg	Asn	Arg	Arg	
							160			165				170		
ctc	acg	gtc	acc	agg	ggt	ttg	caa	aaa	gac	tac	agc	aag	gac	ccg	tgg	685
Leu	Thr	Val	Thr	Arg	Gly	Leu	Gln	Lys	Asp	Tyr	Ser	Lys	Asp	Pro	Trp	
							175			180				185		
cat	ggg	gcc	gag	gtg	tcc	tgc	tgg	ttc	att	cac	aac	aat	ggg	gct	gga	733
His	Gly	Ala	Glu	Val	Ser	Cys	Trp	Phe	Ile	His	Asn	Asn	Gly	Ala	Gly	
							190			195				200		
ctc	atc	gat	ggt	gcc	tac	act	gat	tat	atc	gtc	ccc	gac	atc	ttc		778
Leu	Ile	Asp	Gly	Ala	Tyr	Thr	Asp	Tyr	Ile	Val	Pro	Asp	Ile	Phe		
							205			210				215		
tgagccctct	ggccagcacg	cctgtcctcc	cccgccccca	aggcagagga	ggaggacgac											838
atccgtaccc	gctgctgagg	ctgtacctcc	ttgactaagc	tggcccttg	tgtcaaagca											898
cctcatgcct	tccattaaag	agaggccgtg	tccaaaaaaa	aaaaaaaaaa												947

<210> 52
<211> 239
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..21

<400> 52																
Met	Pro	Leu	Pro	Leu	Pro	Ser	Ala	Phe	Val	Leu	Ser	Ala	Leu	Gln	Pro	
-20						-15					-10					
Ser	Pro	Thr	His	Ser	Ser	Ser	Asn	Thr	Gln	Arg	Leu	Pro	Asp	Arg	Val	
-5						1			5			10				
Thr	Gly	Gly	Phe	Ser	Val	Asn	Gly	Gln	Leu	Ile	Gly	Asn	Lys	Ala	Arg	
						15			20			25				
Ser	Pro	Gly	Gln	His	Asp	Gly	Thr	Tyr	Phe	Gly	Arg	Leu	Gly	Ile	Ala	
						30			35			40				
Asn	Pro	Ala	Thr	Asp	Phe	Gln	Leu	Glu	Val	Thr	Pro	Gln	Asn	Ile	Thr	
						45			50			55				
Leu	Asn	Pro	Gly	Phe	Gly	Pro	Val	Phe	Ser	Trp	Arg	Asp	Gln	Ala		
						60			65			70			75	
Val	Leu	Arg	Gln	Asp	Gly	Val	Val	Val	Thr	Ile	Asn	Lys	Lys	Arg	Asn	
						80			85			90				
Leu	Val	Val	Ser	Val	Asp	Asp	Gly	Gly	Thr	Phe	Glu	Val	Val	Leu	His	
						95			100			105				
Arg	Val	Trp	Lys	Gly	Ser	Ser	Val	His	Gln	Asp	Phe	Leu	Gly	Phe	Tyr	
						110			115			120				
Val	Leu	Asp	Ser	His	Arg	Met	Ser	Ala	Arg	Thr	His	Gly	Leu	Leu	Gly	
						125			130			135				
Gln	Phe	Phe	His	Pro	Ile	Gly	Phe	Glu	Val	Ser	Asp	Ile	His	Pro	Gly	
						140			145			150			155	
Ser	Asp	Pro	Thr	Lys	Pro	Asp	Ala	Thr	Met	Val	Val	Arg	Asn	Arg	Arg	
						160			165			170				
Leu	Thr	Val	Thr	Arg	Gly	Leu	Gln	Lys	Asp	Tyr	Ser	Lys	Asp	Pro	Trp	
						175			180			185				
His	Gly	Ala	Glu	Val	Ser	Cys	Trp	Phe	Ile	His	Asn	Asn	Gly	Ala	Gly	
						190			195			200				

Leu Ile Asp Gly Ala Tyr Thr Asp Tyr Ile Val Pro Asp Ile Phe
205 210 215